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December 19, 2001, 17:00:29; Search time 2253.73 Seconds (without alignments) 1983.487 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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ပ	-	63.2	15.2	734	13	CNS010MP	AL099163 Drosophil
	7	58.8	14.1	1101	13	CNS00Z38	AL097166 Drosophil
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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; Pred. No. 0.008;
43; Mismatches 77; Indels 0
                   171 others
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/plasmid="pbelobAcil"
/db_xref="laxon:7227"
/clone_lib="DrosbAC"
/clone="BACNOIA24"
/note="end : SP6"
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Best Local Similarity 41.9%; Pred. No. 0.051;
Matches 88; Conservative 38; Mismatches 84;
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT CNS00Z38 LOCUS

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Web: www.genoscope.ons.fr.

Web: www.genoscope.ons.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using please BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using please BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp. the same strain used for the BDGP's pland by the coller individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                      from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong, med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ccll_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                      319 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 378
                                                   taattataattataattatataatactgaaaccatggtgccccctgctgctttacatgga 259
                                                                                 875 TWAATATATTTTAATATTAWATMAAATAAWTAAAATWTTTAWTATATWTTTWTAWTTT 934
                                                                                                                                                  935 TKTTATWTTAWDATWWTATTWATATWTATWWATAAAAWWTAAWTWWAWATTTATATAT 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Other GSSs: RPCI-11-281J17.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
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48.5%; Pred. No. 0.21;
tive 1; Mismatches 158;
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/db_xref="GDB:7607752"
/db_xref="taxon:9606"
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/clone_lib="RRCI-11"
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AQ506817.1 GI:4711564
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Best Local S
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Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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/clone_lib="Medicago truncatula BAC library"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Nam. Y-W, Penmetsa, R.V., Endre, G., Kim, D., an
Cook, D.R. 1999. Construction of a bacterial artificial
chromosome library of Medicago truncatula and
identification of clones containing ethylene response
a 19 c 6 g 205 t
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Other name: DK457-L; date: 8/12/99; Submitted to the Database of
Genome Survey Sequences (GSS) on 12/06/99; More information is
available at 'http://chrysie.tamu.edu/medicago'.
Seq primer: S0-BAC-L (AACGCCAGGGTTTTCCCAGTCACGACG)
Class: BAC ends.
                                                                                                   219 ATATATTGATATATATTTATATATATGATATATATATGATATATGTATATATATATATAT 278
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07-DEC-1999
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                                                              Contact: Cook DR
The Crop Biotechnology Center
Texas A&W University
Department of Plant Pathology and Microbiology, Rm 120
Peterson Bidg, College Station, TX 77843-2132, USA
Tel: 409 862 4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, D., Limpens, E., Peng, H., Ellis, L. and Cook, D.R. BAC end sequencing of Medicago truncatula Unpublished (1999)
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1. 421
/organism="Medicago truncatula"
/cullivar="genotype A17"
/db_xref="taxon:3880"
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Query Match

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CNS03D0I 844 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
015L14 of library G from Tetraodon nigroviridis, genomic survey
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Tetracdon nigroviridis

Tetracdon nigroviridis

Tetracdon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Tetracdontidae; Terracdon, Percomorpha; Tetracdontiformes;

Tetracdontidae; Tetracdon, Dessilva, C.; Fizames; C.; Fisher, C.; Bouneau, L.; Billault, A.; Quetler, F.; Saurin, W.; Bernot, A. and

Meissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided by genome wide analysis using
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12.APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a lan
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                 153 taacatctacaaattgccttttcttatcgaccatgtacatcctaccataattatat 212
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/clone="15="G"
/note="Genoscope sequence ID : COBGO15DF07SP1~end
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                          Length 300;
                                                           Indels
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Pred. No. 0.28;
1; Mismatches 142;
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                                Best Local Sim
Matches 140;
                   Query Match
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1 (bases 1 to 300)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ098895 300 bp DNA GSS 27-AUG-1998
8.3050_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo
saplens genomic clone Plate=3050 Col=5 Row=E, DNA sequence.
AQ098895
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                               201 aattataattataattatataatactgaaaccatggtgccccctgctgcttacatggat 260
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                                                                                                                                                                                                                                                                                                                                                        141 caagatgggaattaacatctacaaattgccttttcttatcgaccatgtacatcctaccat
                                           ö
       Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-387
Fax: (206) 616-387
Fax: (206) 616-388
                                       Indels
Score 55.6; DB 13;
Pred. No. 0.24;
1; Mismatches 165;
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/db_xref="taxon:9606"
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Location/Qualifiers
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13.48;
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Class: BAC e
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Query Match
Best Local Similarity
Matches 156; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ745537 845 bp DNA GSS 16-JUL-1999 HS_2272_A2_B12_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2272 Col=24 Row=C, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Fmai: jwallacedu.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2272 row: C column: 24
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Filtaxon:2505 Col=24 Row=C"
/clone=lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                        211 ataattatataatactgaaaccatggtgcccctgctgctttacatggatttctccgcta 270
                                                                                                           158 TGATTTTAATGTTTATGATTTTTTTTTAGAGWTAAGTTATATTTTTTTATTTTTTTA 217
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               Length 844;
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             Score 55.2; DB 13;
Pred. No. 0.26;
                                          7; Mismatches 170;
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             Query Match 13.3%;
Best Local Similarity 46.4%;
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RS Genoscope.

As Direct Submission

As Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Direct Submission

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr : Profession of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR39E17"
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Score 55.2; DB 13;
Pred. No. 0.26;
1; Mismatches 169;
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/note-"end

BASE COUNT ORIGIN

81

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/clone_lib="RPCI-98"
/clone="BACR38J18"
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a 112 c 102 g
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- Wab : www.genoscope.ons.fr)

- Wab : www.genoscope.ons.fr)

- Pab : www.genoscope.ons.fr)

- Determination of this BAC-end sequence was carried out as part of

collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

please see http://www.frutliy.org The BDGP Drosophila

melanogaster BAC : Ibrary was prepared by Kazutoyo Oscogawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

Nr. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNR provided by the BDGP from the

pl and EST libraries. A more detailed description of the library

filters for hybridization from the BACPAC Resource Center can be

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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR8918 of RPCI-98 library from Drosophila melanogaster (fruit
AL076232
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                                                                                                                                                                                                                                                                                                                  141 caagatgggaattaacatctacaaattgccttttcttatcgaccatgtacatcctaccat
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Pred. No. 0.25;
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Best Local Similarity 42.1%;
Matches 144; Conservative
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LOCUS RESULT 10 CNS00JG1

331 909 ORGANISM

AUTHORS TITLE JOURNAL REFERENCE

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L (Wazes I to Jaco),

Genoscope.

Direct Submission

L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster agnome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gaoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, BCORI digestion of Drosophila DNA provided by the BDGP from the Pland EST library is named RPCI-98 and was constructed by partial isogenic strain y2; on bw sp, the same strain used for the BDGP/s and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualiflers

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Drosophila melanogaster
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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   69 others
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Bp 191 91006 EVRz cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence T7 end of BAC: BACR38118 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 ataattataattataataatactgaaaccatggtgccccctgctgcttacatggatttct 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatatgaacat 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                       25 aatcagttattgaaatatttctgaatttaaacttgcatcaataaawttatgtttttgctt 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616 АИИАААТАТИТИАТАТАТАТАТИТИТИТИТИТИТИТАТАТАТАИАААИААААИАА
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 980)
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                                                                                                                                                                                    Length 928;
                                                                                                      191 others
                                                                                                                                                                                                                                  Indels
/organism="Drosophila melanogaster"
/db_xref="laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR27A24"
                                                                                                                                                                                                                             69; Mismatches 141;
                                                                                                                                                                                        DB 13;
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                                                                                                                                                                                    Score 54.8; DI
Pred. No. 0.3;
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                                                                                                      84 g
                                                                                /note="end : T7'
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Drosophila melanogaster
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31.4%;
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Junet Submisted (02-JUN-1999) Genoscope - Centre National de Sequencage : Submisted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Razutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecord idjestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870 WTAATTAATTWTTWTTWTTTTTATWWAAAWWAAAAAAATTTAAACTWGWAAAATATATAA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 ttgaaatatttctgaatttaaacttgcatcaataaawttatgtttttgcttggactataa 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 tttgtatacgtgtatatataccgtataatgtacatatatttatatgaacatgatta 329
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                               Length 980;
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                                                               melanogaster"
                                                                                                                                                                                                                                                                                                                                               13.2%; Score 54.8; DB 13;
43.6%; Pred. No. 0.3;
Live 22; Mismatches 145;
                                                                                                                                                                                                                      ų
                                                                                                                                                                                                                   297
                                                     /organism="Drosophila m
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/clone_lib="RPCI-98"
/clone="BACR38J18"
/note="end:T7"
Location/Qualifiers
                                                                                                                                                                                                                   102 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fruit fly.
Drosophila melanogaster
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Best Local Similarity 43.6%
Matches 129; Conservative
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Tetracdon nigroviridis.
Tetracdon nigroviridis
Tetracdon nigroviridis
Tetracdon nigroviridis
Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Tetracdonitdae; Tetracdon.
Tetracdonitae; Te
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Sost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis genome survey sequence T7 end of clone 249F10 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                          others
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            melanogaster"
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                                                                                                                                                                                                                         Score 54.6; DB 13;
Pred. No. 0.32;
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/organism="Drosophila mv/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BACR29B23"
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llarity 34.3%;
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Matches 128;
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This Sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                       ID : COAG249DC05LP1~end : T7*
t 119 others
                                                                                                                                                                                                                                                                                                                                   Wing R., Close T.J., Kleinhofs A., Wise R., Begum D., Frisch D., Yu Y. Anderson H., Dale J., Henry D., Kernodle S., Palmer M., Rambo T., Saski C., Schwartzbeck J., Simmons J., Chol D.W., Main D., Wood T., "Development of a genetically and physically anchored EST resource for barley genomics";
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                     149 gaattaacatctacaaattgccttttcttatcgaccatgtacatcctaccataattataa 208
                                                                                                                                                                                                                                                                                                                                                                                                        415 GACTAWTAAWWINAWWATTTANNTAWAWNGTTTTWWNTTTWAWAATATAAWATWTWTAT 474
                                                                                                                                                                                                                                                                                29 agitaitgaaataittoigaatitaaactigcaicaataaawitaigittigoitggac 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVSMED0013H16f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMED0013H16f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                              Length 678;
                                                                                                                                                                                                                                                                  Indels
                                                                                         1. 678
/organism="Tetraodon nigroviridis"
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140 c 126 g 167 t 119 c
                                                                                                                                                                                                                                13.1%; Score 54.4; DB 13; 37.2%; Pred. No. 0.38;
                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                                                                                         209 ttataattataataatactgaaaccatggtgcccctgc 246
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                                                                                                                                                                                                                                                            44; Mismatches
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST; 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                         Conservative
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21-DEC-2000 (Rel. 66,
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Best Local Simil
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/tissue_type="Seedling shoot"
/tab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 TITATITGITITITITATITCATATITGATATITIATITATITATITACIATATATITGI 1086
                                                                                                                                                                                                                                                                                                                                        158 tctacaaattgccttttcttatcgaccatgtacatcctaccataattataatta 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 tataatactgaaaccatggtgcccctgctgcttacatggatttctccgctactatttg 277
                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                         Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.9%; Score 53.8; DB 5; Length 1
Best Local Similarity 51.2%; Pred. No. 0.44;
Matches 147; Conservative 1; Mismatches 135; Indels
                                                                                                                                                                                                                                                    BP; 292 A; 22 C; 74 G; 941 T; 8 other;
                                                                                     Location/Qualifiers
Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu
Seq primer: AATACCCTCACTAAAGGG
High quality sequence start: 38
High quality sequence stop: 1204.
                                                                                                                                                                                                                                                    Sequence 1337
                                                                                                              source
                                                                                     Key
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Search completed: December 19, 2001, 17:00:33 Job time: 2275 sec

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189.6 45.6 1303 17 AAT39337 189.6 45.6 3201 12 AAQ14529 189.6 45.6 4832 22 AAH25423 189.6 45.6 4946 18 AAT59331 189.6 45.6 4946 23 AAH25422 189.6 45.6 5349 19 AAV23239 189.6 45.6 5864 17 AAT3939 189.6 45.6 5865 22 AAD06990 189.6 45.6 7566 14 AAQ42160	22 183.6 44.1 1037 11 AAQ04705 USP-Promoter-casse Lagumin-signalpept 24 183.6 44.1 1085 11 AAQ04703 USP-STORMOTER-casse Lagumin-signalpept 24 183.6 44.1 1160 11 AAQ04703 USP-signalpeptide USP-signalpeptide C 25 176.6 42.5 3201 12 AAQ15144 PUSS BE LCG conformation of Lagumin-signalpeptide Right flanking reg puzzi S 20 176.6 35.0 3153 21 AAZ29122 Plasmid DV131 comp Plasmid DV131 comp S 145.6 35.0 3153 21 AAZ29121 Plasmid DV131 comp Plasmid DV133 used C 32 145.6 35.0 3877 21 AAZ29124 Plasmid DV132 used C 33 145.6 35.0 24596 ANN50226 C C Omplete nucleotide D1 35 104.6 25.1 936 22 AAF58254 Oligonucleotide D1 36 104.6 25.1 936 22 AAF58257 Oligonucleotide D1 37 104.6 25.1 936 22 AAF58257 Oligonucleotide D1 37 104.6 25.1 936 22 AAF58257 Oligonucleotide D1 37 104.6 25.1 936 22 AAF58259 Oligonucleotide D2 31 AAZ9124 PAZ9125 Oligonucleotide D1 37 104.6 25.1 936 22 AAF58257 Oligonucleotide D2 0190nucleotide D2 37 AAF58259 Oligonucleotide D2 0190nucleotide D2 0190n	38 104.6 25.1 938 22 AAF\$6255 40 104.2 25.0 936 22 AAF\$6255 41 104.2 25.0 936 22 AAF\$6255 43 104.2 25.0 936 22 AAF\$6257 44 104.2 25.0 936 22 AAF\$6259 44 104.2 25.0 936 22 AAF\$6259 45 104.2 25.0 936 22 AAF\$6259 45 104.2 25.0 938 22 AAF\$6259 45 104.2 25.0 938 22 AAF\$6259 AAD\$6999 standard; DNA; 416 BP. AAD\$6999; 06-AUG-2001 (first entry) Left (3') border flanking region of ellte event MS-B2 MS-B2 ellte event; transgenic Brassica plant; transformale-sterility gene; ds. Chimeric - Agrobacterium sp.	Chimeric - Brassica sp. XX FH Key TT misc_feature 1193 FT misc_feature 194416 FT misc_feature 194416 FT MO200131042-A2. XX PN WO200131042-A2. XX PF 26-OCT-2000; 2000WO-EP10680. XX PR 29-OCT-1999; 99US-0430497. XX
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. QM nucleic search, using sw model Run on December 19, 2001, 17:31:51; Search time 230.16 Seconds (without alignments) 1549.562 Million cell updates/sec	accagctgcatgaacacccaaactcgat 416 apext 1.0 28662619 residues chosen parameters: 1861242 00	Marinum March 100*	Score Score Application Score Score

misc_feature

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                                                                                                       The present invention relates to a transgenic Brassica plant or its seed, calls or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic harasyca plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
The present sequence is left (3') border flanking region of elite event MS-B2.
                                                   by
of
                                                                                                                                                                                                                                                                                                                                                                       61 atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                 Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                      1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc
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                                                                                                                                                                                                                                                     Length 416;
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                                                                                                                                                                                                             Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                                                                                                                 Score 415.6; DB 22;
Pred. No. 1.6e-74;
                                                                                                                                                                                                                                                  ; Db
1.6e-74;
0;
                                                                                                                                                                                                                                        99.9%; Scor.
100.0%; Pred. No. 1...
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                                                                                  Claim 11; Page 52; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD06997 standard; DNA; 415
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  De Beuckeleer
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Best Local Similarity 100.
Matches 416; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               male-sterility gene; ds.
                     WPI; 2001-300517/31.
  Weston B,
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The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                            Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 415;
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
  1..234
//rtag= a
//note= "Corresponds to plant DNA"
235..415
                                          /*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                  Claim 11; Page 51; 53pp; English.
                                                                                                                                                   (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                            26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                       91.5%;
                                                                                                                                 99US-0430497
                                                                                                                                                                     Weston B, De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                      404; Conservative
                                                                                                                                                                                         WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                      WO200131042-A2
                                                                                                                               29-OCT-1999;
                               misc_feature
                                                                                          03-MAY-2001
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Best Local 9
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Matches
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21-FEB-1996;
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AAD06990
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                                                                                                                                                                                                                                                                                                               /note= "region containing polyA signal of nopaline synthase gene of Agrobacterium T-DNA" complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                         /note= "Bacillus amyloliquefaciens barnase coding
                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                             Plasmid pTCO113 T-DNA used to obtain male sterile oilseed rape.
                                                                             Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar; transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                                                                                /*tag= g
/label= PTA29
/note= "promoter of stamen-specific TA29 gene
Nicotiana tabacum"
                                                                                                                                                                                                                                                                       /note= "promoter of Arabidopsis Rubisco small subunit gene" complement (2659..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "promoter of nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "region coding for barstar of Bacillus
                                                                                                                                                     /note= "right border of Agrobacterium T-DNA" complement (98..330)
                                                                                                                                                                                                                               /note= "region coding for phosphinothricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "left border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= j
/label= 3'g7
/note= "region containing polyA signal of
of Agrobacterium T-DNA"
complement (5840..5864)
                                                                                                                                                                                     /note- "region containing polyA signal of of Agrobacterium T-DNA" complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amyloliquefaciens"
                                                                                                                                                                                                                                      acetyltransferase"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                  region"
complement (3368..4877)
                                                                                                                      Location/Qualifiers complement (1..25)
              AAT39339 standard; DNA; 5864 BP.
                                                                                                                                                                                                                                                                                                                                          /*tag= f
/label= Barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Barstar
                                                                                                                                                                                                                                                                                                 /*tag= e
/label= 3'nos
                                                                                                                                                                                                                                                         /*tag= d
/label= Pssu
                                                                                                                                                                       /*tag= b
/label= 3'97
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/label= Pnos
                                                                                                                                                                                                                 /*tag= c
/label= bar
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                                             (first entry)
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/label= I
                                                                                                                     Key
misc_feature
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                                                                                                                                                               polyA_signal
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                                             22-JAN-1997
                                                                                                     Synthetic.
                             AAT39339;
                                                                                                                                                                                                                                                promoter
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     AAT39339
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29-AUG-1996

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T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                           plasmid prcoll3 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-regulatory) gene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using prcoll3 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of barstar counteracted any low level expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                                                         Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.3%; Score 192.6; DB 17; Length 5864; 99.5%; Pred. No. 4.6e-30; Artive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                                                                                                                                                                                                                                                                                     Example 3; Page 33-3743-47; 56pp; English.
                                                                                                                           Ē
                                                                                                                           Michiels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - Streptomyces hygroscopicus.
Chimeric - Arabidopsis thaliana.
Chimeric - Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Nicotiana tabacum.
Chimeric - Agrobacterium tumefaciens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric T-DNA of plasmid pTC0113.
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                                                                                GENETIC SYSTEMS
                                                                                                                           Cornelissen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD06990 standard; DNA; 5865
                                        95EP-0400364.
96WO-EP00722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.54
Matches 192; Conservative
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                                                                                                                                                                     WPI; 1996-402373/40.
                                                                                (PLBZ ) PLANT
                                                                                                                             Botterman J,
                                          21-FEB-1995;
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3'UTR

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The present invention relates to a transgenic Brassica plant or its seed cells or tissues, characterised by harbouring a specific seed cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Transgenic Location in the Brassica genome. Transgenic transgenic plant with a male-fertile Brassica plant and harvesting the transgenic plant with a male-fertile Brassica plant and harvesting the Thyprid seed from the transgenic Brassica plant.

The present sequence is chimeric T-DNA of plasmid procil3. This sequence region (UTR) from TL-DNA of PriBGS3, synthetic polylinker sequences region (UTR) from TL-DNA of PriBGS3, synthetic polylinker sequences. Streptomyces hygroscopicus, barnase gene from Bacillus amyloliquefaciens and barsetar gene from Bacillus amyloliquefaciens and barsetar gene from Bacillus amyloliquefaciens and barsetar gene from macillus amyloliquefaciens and barsetar sequences. Arabidopsis thalians, the anther-specific gene TA29 from Nicotiana tabacum and nopaline synthase gene from the T-DNA of priB37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome.
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/note= "Residual sequence from the TL-DNA at the
right border repeat"
5811.5840
/*tag= w
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc
                                                                                                                                                                                                                                                                                                                                         /*tag= x
/note= "Left border repeat from the TL-DNA from
                                                                                   /*tag= u
/note= "Synthetic polylinker derived sequence"
5774..5810
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46.3%; Score 192.6; DB 22; Length 5865;
Best Local Similarity 99.5%; Pred. No. 4.6e-30;
Matches 192; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                        gene 7 (3'g7) of primess"
5767..5773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 47-49; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-2000; 2000WO-EP10680
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/note= "TagI fragment from the 3' untranslated end of the nopaline synthase gene (3'nos) from the T-DNA of prim37 and containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/note= "Promoter from the atSlA ribulose-1,5-biphosphate
carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= o /*tag= o /*tag= nometer of the nopaline synthase gene from the folds. 521% of Agrobacterium tumefaciens" factor folds: 5216..5217 /*tag= p //*tag= 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- k
/note= "The 3' untranslated region downstream from the
barnase coding sequence of Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= m
/note= "Promoter region of the anther-specific gene
/29 from Nicotlana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Protein encoded by bialaphos resistance
gene (bar) of Streptomyces hygroscopicus"
884..2609
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1..25
//ortsg- a
//ortsg- "Right border repeat from the TL-DNA from
p_T1B653"
                                                                                                                                                                                                                                                                   /*tag= d
/note= "The 3' untranslated end from the TL-DNA
310..33
                                                                                                                         '*tag= b
'note= "Synthetic polylinker derived sequence"
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/product Protein encoded by barnase gene from 3369..4878
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag- e
/note- "Synthetic polylinker derived sequence"
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/note= "Synthetic polylinker derived sequence"
2660..2920
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2937..3032
                                                                                                                                                                                                     /*tag= c
//note= "Residual sequence from the TL-DNA at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= t
/note= "The 3' untranslated end from the TL-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= n
/note= "Synthetic polylinker derived sequence"
4925..5215
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/note= "Sequence from the 3' untranslated end
barstar gene from Bacillus amyloliquefaciens"
5531..5554
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/product= "Protein encoded by barstar gene of
Bacilius amyloliquefaciens"
5491..5530
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//orte= "synthetic polylinker derived sequence"
//orfe= "synthetic polylinker derived sequence"
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misc_feature
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The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                              Male sterile plant; RNAase inhibitor; plasmid pTS172delta; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14-17; 29pp; Japanese.
                                                            AAF86439 standard; DNA; 5228
                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0279307.
                                                                                                                                                                                                                                                                                                                                                                12-SEP-2000; 2000WO-JP06222.
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (NISB ) JAPAN TOBACCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamada K, Nakakido F;
                                                                                                                                                                         Plasmid pTS172delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-266212/27
                                                                                                                                                                                                                                                                                        WO200124616-A1
                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1999;
                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                    25-JUN-2001
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                                                                                                 AAF86439
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                                      AAF86439
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                                                                                                                                                                                                                                                                                      Plant promoter; root cell; root-specific expression; parasite resistance; nematode resistance; fungal resistance; water stress; salt stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a plasmid PGKB5. The plasmid contains a plant promoter that directs expression of a selected sequence in root cells at all stages of development of a plant. The plant promoter is used to control expression of genes in a root-specific manner, especially genes that provide resistance to parasites, pests (nematodes or fungi), water and salt stress, or alter sugar content or nitrogen transport. Fragments of the promoter are useful as probes or primers to detect or amplify at least part of the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New constitutive plant promoter active specifically in roots, useful for controlling expression of pest or drought resistance genes, and related transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 46.3%; Score 192.6; DB 22; Length Best Local Similarity 99.5%; Pred. No. 4.6e-30; Matches 192; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                 Nucleotide sequence of a plasmid PGKB5
                                                                                                                                                                                                                                                                                                                           sugar content; nitrogen transport; ss
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                                                                                                                                    AAF25320 standard; DNA; 7599 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-FR01768
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                                                                                                                                                                                                                (first entry)
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                                        5801 gaccatgtacatc 5813
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                                                                                                                                                                                                            30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                             1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60
                                                       ő
                                  Length 5228;
Sequence 5228 BP; 1384 A; 1307 C; 1263 G; 1274 T; 0 other;
                                                       Indels
                                45.7%; Score 190; DB 22; 99.0%; Pred. No. 1.5e-29; tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                            6233
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                                                       Matches 190; Conservative
                                                                                                                                                                                                                                                                                           AAZ91097 standard; DNA;
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                                             Best Local Similarity
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rice; Oryza
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                                               Key
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                                                                                                                                                                                                             Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undesirable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                                                                                                                                    6342 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pTS174; male sterile; barnase; ribonuclease; transgenic plant;
                                                                                                                                                                                                                                                                  The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AAZ91095) for expression appecifically in the anther of a plant. This sequence represents the E. coll/Agrobacterium shuttle vector plasmid pTS172 which contains the mutated barnase gene (AAZ91095) under control of the cauliflower mosale virus 355 promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atcaataaawttatgttttgcttggactataatacctgacttgttattttatcaataaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatitaaactatatttctttcaagatgggaattaacatctacaaattgcctttcttatc 180
                            Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
         coli plasmid pTS431 containing mutant barnase gene.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 190; DB 21;
Pred. No. 1.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pTS174 used to obtain male sterile rice.
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                Example 3; Page 23-27; 30pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT39336 standard; DNA; 6548 BP.
                                                                                                                                    98JP-0220060.
                                                                                                                  99WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                     (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                         Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 gaccatgtacat 192
                                                                                                                                                                                           WPI; 2000-195581/17.
                                                                           WO200008176-A1.
                                                                                                               03-AUG-1999;
                                                                                                                                   04-AUG-1998;
                                                                                             17-FEB-2000
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                                                                                                                                                                        Hamada K,
                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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XID AAT3
XX AC AAT3
XX DT 22-J
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XX XX KW Plas
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Plasmid pTS174 (AAT39336) contains Bacillus barnase DNA under control of the stamen-specific PEI promoter. Embryogenic callus from rice v. Kochinbikis was transformed with pTS174 alone or with pTS88 (see also AAT39337), a plasmid contg. barstar DNA under control of a 15S promoter. With pTS174 alone, I male sterile line was recovered from 48 electroporation cuvettees. With both plasmids, 7 normal male sterile lines were recovered from 40 cuvettes. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function= region containing polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                 polyadenylation signal gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function= promoter of the stamen-specific El
                                                                                                                                                                                                                                                                                                                                                                                              /product= Bacillus amyloliquefaciens barnase complement (2625..4313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphinothricin acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6548 BP; 1757 A; 1578 C; 1523 G; 1690 T; 0 other;
                                                                                       /*tag= a
//tag= vactor
/label= Vector
/note= "pUC19 derived vector sequences"
complement (2019..2283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                            /note= "region containing
nopaline synthase
T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                      complement (2284..2624)
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                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
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/label= P35S
/function= 35S p
5711..6262
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/label= Barnase
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/label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= PE1
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/label= bar
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6263..6496
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                                                                             1..2003
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                                                                       misc_feature
                                                                                                                                                                         polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9626283-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Botterman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1996
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
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Length 6548;

DB 17;

45.7%; Score 190;

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De Block M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ91096
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                                                                                                                                                         6470
                                                                                                                                                                                      Gaps
                                                                                                                                         1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "35S promoter region of cauliflower mosaic virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "3' untranslated region contg. the poly-A signal of Agrobacterium T-DNA nopaline synthase gene" complement (2289..2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                '3' untranslated region contg. the poly-A signal of gene 7 of Agrobacterium T-DNA"
                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "phosphinothricin acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plant; poly-(ADP-ribose) polymerase inhibitor;
niacinamide; Agrobacterium; T-DNA; male sterile; barnase;
ribonuclease; RNase; cereal; wheat; Triticum aestivum;
                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "promoter region of rice El gene"
complement (4336..5710)
   Pred. No. 1.5e-29;
                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product barnase complement (2625..4313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2019..2288)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa;
cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                   AAT61394 standard; DNA; 6548 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= 3'g7
99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Agrobacterium sp.;
Chimeric Oryza sativa;
Chimeric cauliflower mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95EP-0401844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- PE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..6496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5711..6262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= d
/label= P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1997 (first entry)
                   Matches 190; Conservative
                                                                                                                                                                                                                                                                                            6531 gaccatgtacgt 6542
                                                                                                                                                                                                                                                               gaccatgtacat 192
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid pTS172; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP757102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                     AAT61394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promote
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3'UTR
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                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                    AAT61394
                                                                                                                                                                                                                                                                                                                                                    RESULT
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plasmid pTS172 (AAT61394) contains the barnase coding sequence under control of the rice El gene stamen-specific promoter and a phosphinothricin acetyltransferase coding sequence under control of the CaWW 35S promoter. Plasmid pTS172 and plasmid pTS772 (see also AAT61395) were used to transform wheat Spring variety Pavon calli via particle bombardment. Some calli were treated with the poly-(ADP-ribose) polymerase inhibitor niacinamide before, or before and after, bombardment. Healthy, male sterile plants were regenerated only from bombarded calli that were treated with niacinamide. This was believed to be due to more faithful expression characteristics of the integrated stamen-selective batnase gene in these callicated profits. For plants transformed with pTS172, copies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6351 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                                                                                         Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and \phantom{a}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 190; DB 18; Length 6548;
Pred. No. 1.5e-29;
1; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli plasmid pTS172 containing synthetic barnase gene
                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 17-20; 25pp; English
                                                                (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ91096 standard; DNA; 6548 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative 1
95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 gaccatgtacat 192
                                                                                                                                                                                           WPI; 1997-111050/11.
                                                                                                                                                                                                                                                                                                                          reduces metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200008176-A1.
04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-2000
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Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                  δ
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                                                                                                                                                                                                                                                                                                                                                      The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AAZ91095) for expression specifically in the anther of a plant. This sequence represents the E. coll/Agrobacterium shuttle vector plasmid pTS172 which contains the synthetic barnase gene (AAZ91094) under control of the cauliflower mosaic virus 35S promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                                                                                                                                                                                                      Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undestrable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Male sterile plant; RNAase inhibitor; plasmid pTS346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 190; DB 21;
Pred. No. 1.5e-29;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                              Example 3; Page 19-23; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF86441 standard; DNA; 7492 BP.
                                            98JP-0220060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
  99WO-JP04167
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                                                                                       (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISB ) JAPAN TOBACCO INC.
                                                                                                                                      Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6531 gaccatgtacgt 6542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 gaccatgtacat 192
                                                                                                                                                                              WPI; 2000-195581/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pTS346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200124616-A1.
                                          04-AUG-1998;
03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3T-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2001
                                                                                                                                      Hamada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF86441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
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ID AAF8
XX
AC AAF8
XX
DT 25-J
XX
XX
DE Plas
XX
XX
MA16
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MA20
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plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                 tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc 180
                                                                                                                                    present invention relates to a method for producing male sterile
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                         Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function= 35S promoter of cauliflower mosaic virus strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                              Length 7492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/label= barstar
/product= Bacillus amyloliquefaciens barstar
968..1287
/*tag= d
                                                                                                                                                                                                                                                         Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                         Score 190; DB 22;
Pred. No. 1.5e-29;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= pgem2
/note= "polylinker of pgem2"
                                                                                                    Disclosure; Page 19-23; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 1..35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT39337 standard; DNA; 1303 BP.
                                                                                                                                                                                                                                                                                                          45.7%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/label= P35S
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.0°
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695..967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 694
Hamada K, Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7475 gaccatgtacgt 7486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaccatgtacat 192
                              WPI; 2001-266212/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyA_signal
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181
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                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                        jion containing polyadenylation signal gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                          The HindIII-EcoRI fragment (AAT39337) of plasmid pTS88 contains barstar DNA under control of a 35S promoter. The plasmid was used with pTS14 (see also AAT39356) contq. barnase DNA under control of the stamen-specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVEI36 (see also AAT39338) contg. barnase DNA under control of the stamen-specific PCA55 promoter to produce male sterile maize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible lqw level expression of barnase DNA in non-stamen tissue.
                                                                                                                                                                                              Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                     ; DB 17; Length 1303;
.7e-29;
es 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                           Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                     PGEM2
                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Score 189.6;
Pred. No. 1.7
                                                                                                                                                            Cornelissen M, Michiels F;
                                    /*tag= e
/label= pGEM2
/note= "polylinker of
          region
                                                                                                                                                                                                                                          Example 1; Page 38; 56pp; English
                                                                                                                                           GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                   oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pPS029 Bt ICP coding sequence
                                                                                                                                                                                                                                                                                                                                                                                      45.6%;
/label= 3'q7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ14529 standard; DNA; 3201
                                                                                                        96WO-EP00722
                                                                                                                         95EP-0400364
         /function=
                          1288..1303
                                                                                                                                                                                                                                                                                                                                                                                                     Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1278 gaccatgtac 1287
                                                                                                                                                                              NPI; 1996-402373/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 gaccatgtac 190
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                           (PLBZ ) PLANT
                          misc_feature
                                                                                                                                                             Botterman J,
                                                                                                        21-FEB-1996;
                                                                                                                         21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1992
                                                                                      29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ14529
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ID AAQ1
XX
AC AAQ1
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hybrid seed; male-sterility gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "n" in the sequence refers to not known nucleotides. pPS029 is identical to pVE36 (AAQ15144), but carries both the aminoterminal modification and the internal modification of the Bt ICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.6%; Score 189.6; DB 12; Length 3201; illarity 99.5%; Pred. No. 1.8e-29; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                 Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
thuringiensis; insecticidal crystal protein;
                                                                                                                                                                                                                                                                                                                  Dockx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plant; winter oilseed rape; fertility restorer gene; barstar gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of plasmid pTHW118
                                                                                                                                                                                                                                                                                                                  Stam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6(c); 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also AAQ14529, AAQ15142-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH25423 standard; DNA; 4832
                                                                                                                                                                                          91WO-EP00733.
                                                                                                                                                                                                                               90EP-0401055
                                                                                                                                                                                                                                                                                                                  Cornelissen M, Soetaert P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces hygroscopicus.
Arabidopsis thaliana.
Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                        GENETIC SYST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3132 gaccatgtac 3141
                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-339820/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaccatgtac 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sednence
                                                                                                                                                                                                                                                                        (PLAN-) PLANT
                   deletion; ss
                                                                                                                                                                                       17-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2001
                                                                                                    WO9116432-A
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                                                             Synthetic.
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07-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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                                                          a
"right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                         /note= "atsla ribulose-1,5-biphosphate carboxylase
small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= p
/note= "left border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= j /note= "Taq1 fragment from 3' UTR of nopaline synthase gene from T-DNA of pTIT37 and containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "downstream of Bacillus amyloliquefaciens
barstar coding region"
complement (2981..3253)
                                                                                                                                                                                                                                                                   /*tag= f
/*tag= f
/note= "synthetic polylinker derived sequences"
complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= m
/note= "Barstar gene coding region from Bacillus
amyloliquefaciens"
                                                                                             /*tag= b
.note= "synthetic polylinker derived sequences"
                                                                                                                                                                                      /*teg= d
/note= "synthetic polylinker derived sequences"
complement (98..309)
                                                                                                                                     /*tag= c
/note= "residual sequence from TL-DNA at right
                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= 1
/note= "synthetic polylinker derived sequences"
complement (2659, 2919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note- "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= n
/note= *anther-specific gene TA29 promoter from
Nicotiana tabacum"
4763..4807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- o
/note= "synthetic polylinker derived sequences"
8688..4832
                                                                                                                                                                                                                                 /*tag= e
/note= "3' UTR from TL-DNA gene 7 of pTiB6S3"
                                                                                                                                                                                                                                                                                                            /*tag= g
/note= "Streptomyces hygroscopicus bialaphos
resistance (bar) gene"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3254..4762)
                                                                                                                                                                 border repeat
                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                        ..2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2000; 2000WO-EP12872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0457037
                                                                                                                                                                                                                                                         310..330
                                                                                  26..53
/*tag=
                                                                     'note-
                                                                                                                        54..90
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                              91..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-381419/40.
Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200141558-A1
                                                                                misc_feature
                                         misc_feature
                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Both G,
                                                                                                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                   3'UTR
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                          Key
                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is seed have agronomic performance, genetic stability and adaptability to plasmid parent generic backgrounds. The present sequence represents replaying plasmid comprises the barstar gene, which acts as a fertility restorer gene. The plasmid is used to create transgenic
Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 tatttaaactatatttcttcaagatgggaattaacatctacaaattgcctttcttatc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP; nlacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; oilseed rape; Brassica napus;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 189.6; DB 22; Length 4832;
Pred. No. 1.8e-29;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                '3' untranslated region contg. the poly-A signal of gene-7 of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                   Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= RB
/note= "T-DNA right border"
complement (97..330)
                                                                         Example 1; Page 80-82; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers complement (1..25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric Agrobacterium sp.;
Chimeric Arabidopsis thaliana;
Chimeric Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT59531 standard; DNA; 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/label= 3'97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-DNA of plasmid pTHW107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 gaccatgtac 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid pTHW107; ds.
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plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a barnase coding sequence under control of the tobacco TA29 gene stamen-specific promoter and a phosphinothricin accepyltransferase coding sequence under control of an Arabidopsis Rubisco small subunit gene promoter. Oilseed rape hypocotyl explants were infected with Agrobacterium tumefaciens CS8CIRMf carrying vector PTHW107 and helper Ti plasmid pWF60. In some treatments, the hypocotyls were treated with the poly-(AAD-ribose) polymerase inhibitor niacinamide (250 mg/1) 4 days prior to infection. Plants regenerated from niacinamide-treated transformed calli expression profile of the transgenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and reduces metabolism
                                                                                           /note= "promoter region of Rubisco small subunit
gene of Arabidopsis thaliana"
complement (2658..3031)
                                                                                                                                                               /note= "3'untranslated region contg. the poly-A
                                                                                                                                                                             signal of the nopaline-synthase gene of
Agrobacterium T-DNA"
complement (3032..3367)
                                                                                                                                                                                                                                                                                                      /note= "promoter region of tobacco TA29 gene"
complement (4822..4946)
                                    /product- phosphinothricin acetyltransferase complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                          /note= "T-DNA left border"
                                                                                                                                                                                                                                              /product= barnase
complement (3368..4876)
 complement (331..882)
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 13-16; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENETIC SYSTEMS NV
                                                                                                                                                                                                                      /*tag= f
/label= Barnase
                                                                                                                                                                                                                                                                                        /label= PTA29
                                                                     /*tag= d
/label= PSSU
                                                                                                                                                                                                                                                                                                                                                                                                                                         95EP-0401844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95EP-0401844
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/label- LB
                                                                                                                                        /*tag= e
/label= 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-111050/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLBZ ) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                     EP757102-A1
                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De. Block M;
                                                       promoter
                                                                                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                                                                   misc_RNA
                                                                                                                       3'UTR
Ços
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Search completed: December 19, 2001, 17:32:10 Job time: 4167 sec
                                          gaccatgtac 190
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                                           181
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Gaps

61 atcaataaawttatgttttgcttggactataatacctgacttgttattttatcaataaa 120

1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60

g

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Query Match 45.6%; Score 189.6; DB 18; Length 4946; Best Local Similarity 99.5%; Pred. No. 1.8e-29; Matches 189; Conservative 1; Mismatches 0; Indels 0;

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December 19, 2001, 17:27:49; Search time 1631.12 Seconds (without alignments) 4207.432 Million cell updates/sec
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1 ctacggcaatgtaccagctg.....catgaacacccaaactcgat 416
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1472140 seqs, 8248589755 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_Vico_lnu: *
em_htgo_lnu: *
em_htgo_lnu: *
em_htg_hum: *
em_htg_lnu: *
em_htg_lnu: *
em_htg_loid: *
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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				PAT	ds for t"
AA12/748 AX063413 E31991 A60109 A76916 AR088308 E31990	ARO78675 ARO78675 AXA12441 AA0108 A76915 ARO98307 AXI72440 A71437 A60112	AX127748 AX127748 A24783 AR074386 AR074387 A10942 A10943 AX172463	TB1251013 TB1251014 A18051 AR095107 AR098313 AX012338 149886 129886 123374 BINNYGDNA ATTEN7 A	ALIGNMENTS DNA ent WO0131042.	synthetic construct. synthetic construct artificial sequence. 1 (bases 1 to 416) Weston, B. and de Beuckeleer, M. Male-sterile brassica plants and methods i Patent: WO 0131042-A 10 03-MAY-2001; Aventis CropScience N.V. (BE) Location/Qualifiers 1416 /db_xref="faxon:32630" //db_xref="faxon:32630" //ote="3' border flanking region
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AX127748
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/note="5' border flanking region of
                                                                            DB 6;
1.4e-63;
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Pred. No. 3.7e-57;
1; Mismatches 3;
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( synthetic construct
artificial sequence.

1 (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methor Pertent: WO 0131042-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
                                                                        99.9%; Score 415.6;
100.0%; Pred. No. 3.4
tive 0; Mismatches
                                         152
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Sequence 8 from Patent WO0131042.
AX127755
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                      194. 416
/note="plant DNA"
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1. .193
/note="T-DNA"
194. .476
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/note="T-DNA"
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Best Local Similarity 98.5%;
Matches 404; Conservative
                                                                       Query Match
Best Local Similarity 100.
Matches 416; Conservative
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                       misc_feature
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TITLE
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1; Mismatches 0;
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/db_xxef-"taxon:32630"
/loce-"T-DNA of plasmid pcoll3"
/ 1095 c 1149 g 1772 t
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Sequence 1 from Patent W00131042.
AX127748
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Best Local Similarity 99.5
Matches 192; Conservative
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1 (bases 1 to 6548)
De, B.M.
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Best Local Similarity 99.08
Matches 190; Conservative
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Plasmid PTS172
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C12N15/09,A01H5/00,C12N5/10,C12N9/22//(C12N5/10,C12R1:91), PC
                                                                                              synthetic construct.
synthetic construct
synthetic construct
a stificial sequence.
1 (bases 1 to 7599)
Hoffmann, B., Mollier, P. and Pelletier, G.
Promoter expressed specifically in the cells of plant roots,
Promoter expressed specifically in the cells of plant roots,
promoter expressed specifically in the cells of plant roots,
promoter expressed specifically in the cells of plant roots,
plants obtained
Patent: WO 0100833-A 5 04-JAN-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                     24-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                   Length 7599;
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Pred. No. 1.3e-24;
1; Mismatches 0; Indels
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E31991
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Mutated barnase gene and transgenic plant thereof
Patent: JP 2000041682-A 4 15-FEB-2000;
                                     PAT
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/db_xrs0n:32630"
// 1938 c 1937 g 1752 t
                                   AX063413 7599 bp DNA
Sequence 5 from Patent WO0100833.
AX063413
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                                                                                                                                                                                                                        Location/Qualifiers
1. .7599
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JP 2000041682-A/4
                                                                       AX063413.1 GI:12541201
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Best Local Similarity 99.5%;
Matches 192; Conservative
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Location/Qualifiers
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                                                                                                                                              Length 6539;
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Pred. No. 3.6e-24;
1; Mismatches 1; Indels
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Location/Qualifiers
1. 6548
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Sequence 2 from Patent W09706267.
A60109
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                                                                 /organism="unidentified"
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1579 c 1523 g 1
                                                                             /db_xref="taxon:32644"
1578 c 1519 g 1
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DEFINITION ACCESSION VERSION KEYWORDS

RESULT A76916 LOCUS

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SOURCE

AUTHORS TITLE JOURNAL

FEATURES

REFERENCE

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KAZUYUKI HAMADA, FUMIO NAKAKIDO
C12N15/09,A01H5/00,C12N5/10,C12N9/22//(C12N5/10,C12R1:91), PC
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                                           1. .6548 // /
/organism='Escherichia coli LE392'
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Mutated barnase gene and transgenic plant thereof
Mutated barnase gene and transgenic plant thereof
Patent: JP 2000041682-A 3 15-FEB-2000;
JAPAN TOBACCO INC
OS Escherichia coli LE392
PN JP 2000041682-A/3
PD 15-FEB-2000
PF 04-AUG-1998 JP 1998220060
PR KAZUYUKI HAMADA, FUMIO NAKAKIDO
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Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels
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/organism="unidentified"
/db_xref="taxon:32644"
a 1579 c 1523 g 169(
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Pred. No. 3.6e-24;
1; Mismatches 1; Indels
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Patent: US 6074876-A 2 13-JUN-2000;
Location/Qualifiers
1. 6548
                                                   A/O916 6548 bp DNA circular PAT
Sequence 2 from Patent EP0757102.
A76916
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Pred. No. 3.6e-24;
1; Mismatches 1;
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/organism-"Plasmid PTS172"
/db_xref="taxon:106340"
1579 c 1523 g 1690 t
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AR098308
AR098308.1 GI:12807565
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1 (bases 1 to 6548)
De,B.M.
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De Block, M.
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Matches 190; Conservative
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AR098308 LOCUS DEFINITION

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181

VERSION KEYWORDS SOURCE ORGANISM

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3012 ATCAATAAATTTATGTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 3071
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                                                                                                                                                                                                                                                                   synthetic construct.
synthetic construct
artificial sequence.
[1] (bases 1 to 4832)
de Both,G. and de Beuckeleer,M.
Hybrid winter oilseed rape and methods for producing same patent: WO 0141558-A 2 14-JUN-2001;
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/db_xref="taxon:33530"
/note="rDNA of plasmid pTHW118"
1883. 4065
/note="Hpal restriction fragment"
a 883 c 932 g 1488 t
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Pred. No. 4.3e-24;
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Sequence 2 from Patent WO0141558.
AX172441
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Sequence 1 from Patent W09706267
A60108
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pTHW107
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1 (bases 1 to 4946)
De, B.M.
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Best Local Similarity 99.5%;
Matches 189; Conservative 1
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Cornelissen,M., Soetaert,P., Stam,M. and Dockx,J.

Modified Bacilius thuringlensis insecticidal-crystal protein genes and their expression in plant cells
Patent: US 5633446-A 23 27-MAY-1997;

Location/Qualifiers
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                                  31-AUG-2000
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Cornelissen,M., Reynaerts,A., Gossele,V. and Van Aarssen,R.
Marker gene
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                                                                                                                                                                                 Patent: US 5962768-A 5 05-OCT-1999,
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144104
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1. .7811
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710 c 720 g
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1906 c 1873 g
                               AR078675 7811 bp DN
Sequence 5 from patent US
AR078675
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449 GACCATGTACGT 438
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Best Local Similarity
Matches 189; Conserv
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PLANT GENETIC SYSTEMS NV (BE)
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                        Query Match 45.6%; Score 189.6; DB 6; Best Local Similarity 99.5%; Pred. No. 4.3e-24; Matches 189; Conservative 1; Mismatches 0;
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Transformation vector pTHW107
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De Block,M.
Genetic transformation using a PARP inhibitor
Patent: US 6074876-A 1 13-JUN-2000;
Location/Qualifiers
1. .4946
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Sequence 1 from patent US 6074876.
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US-08-973-73-4
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-894-440-1
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Listing first 45 summaries

    nucleic search, using sw model

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RESULT 1

US-08-991-40-4

US-08-901-40-4

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INFORMATION: of nopaline synthase gene of Agrobacterium
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; Patent No. 6074876
; GENERAL INFORMATION:
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Best Local Similarity 99.08
Matches 190; Conservative
                                                    NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LENGTH: 6548
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OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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LOCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
                                                                                      NAME/KET: misc_feature

LOCATION: (4924)..(5216)

OTHER INFORMATION: promoter of nopaline synthase gene of
OTHER INFORMATION: Agrobacterium T-DNA (Phos)

FEATURE:
NAME/KEY: misc_feature
LOCATION: (5217)..(5489)

OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
COCATION: (5490)..(5765)

OTHER INFORMATION: region containing polyadenylation signal of contex information: cegion containing polyadenylation signal of contex information: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.3%; Score 192.6; DB 3; Length 5864; 99.5%; Pred. No. 1.4e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08894440
| Patent No. 6025546
| GENERAL INFORMATION:
| TILLE OF INVENTION: Method to obtain male sterile plants
| FILLE REPERENCE: NMSCOR
| CURRENT FILING DATE: 1997-11-12
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: Patentin Ver. 2.0
| LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 192.0, Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)..(2003)
OTHER INFORMATION: pUC19 derived vector sequences
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5800 gaccatgtacatc 5812
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NAME/KEY: misc_feature
LOCATION: Complement(()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-894-440-4
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US-08-894-440-1
                                                                              FEATURE:
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61 atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
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                                                                                                                                                                                                                                                                                                                                                        CCATION: (5711). (6262)
CTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (6263)..(6496)
OTHER INFORMATION: region containing polyadenylation signal fo gene 7
US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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NAME/KEY: misc_feature
                                                                                                                                                                  gene of rice
                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DE BLOCK,
ARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER APPLICATION NUMBER: PP 95401844.6
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 190; DB 3; Length 65
Pred. No. 5.7e-35;
1; Mismatches 1; Indels
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                 NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El
OTHER INFORMATION: (PEI)
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121 tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "the 3' end formation and polyadenylation region of T-DNA gene
CURRENT APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US/08/549,680A
FILING DATE: 16 JANUARY 1996
CLASSIFICATION: 800
FTORMEY/AGENT INFORMANDER
NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: /note= "T-DNA left border; OTHER INFORMATION: sequences" US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 190; DB 2;
ilarity 99.0%; Pred. No. 5.8e-35;
Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label= vector pTRVA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: promoter
LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-0111P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                         TELEX: 248345;
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                    (703) 205-8000
(703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 484..684
OTHER INFORMATION: /not
OTHER INFORMATION: poly
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Best Local Similarity
Matches 190; Conserv
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                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . LOCATION: (6263)..(6496)
. OTHER INFORMATION: 3'97: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium US-08-817-188-2
                                                     LOCATION: Complement((2019)..(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA.
                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
COGATION: (4336)..(5170)
OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.7%; Score 190; DB 3; Length 6548; 99.0%; Pred. No. 5.7e-35; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CORNELISSEN, MARCUS
APPLICANT: CORNELISSEN, MARCUS
APPLICANT: REYNERTS, ARLETTE
APPLICANT: WAN ARSSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUWTRY: User.
                                                                                                                                                                                                                                                                                         gene of
                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LCCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                       臣
                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: PE1: promoter region of
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: Complement((5711)..(6262))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-549-680A-5/c

; Sequence 5, Application US/08549680A

; Patent No. 5962768

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.0
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6531 gaccatgtacgt 6542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
CCATION: 2078..2082
COTHER INFORMATION: /note- "Nucleotides 2078-2082
CTHER INFORMATION: wherein N is not known."
US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY_AGENT_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       010830-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Red, Teresa S
REGISTRATION NUMBER: 30,427
REPRENCE/DOCKET NUMBER: 0108:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEO ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3132 GACCATGTAC 3141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (968]..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI OTHER INFORMATION: fragment of prs88
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Caulifidwer Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (695)..(957)
OTHER INFORMATION: region coding for barstar of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1303;
Sequence 2, Application US/08894440

Patent No. 6025546

GENERAL INFORMATION:
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REPERENCE: NASCOR
CURRENT APPLICATION NUMBER: US/08/894,440

CURRENT FILING DATE: 1997-11-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 5EQ ID NOS: 4

LENGTH: 1303
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45.6%; Score 189.6; DB 3;
Best Local Similarity 99.5%; Pred. No. 6e-35;
Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)..(35)
OTHER INFORMATION: POLYLINKER of PGEM2 (PGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature

: LOCATION: (1288)..(1303)

: OTHER INFORMATION: polylinker of pGEM2

US-08-894-440-2
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US-08-453-104-23
US-08-453-104-23
Sequence 23, Application US/08453104
Patent No. 5633446
CENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: STAM, Malke
APPLICANT: STAM, Malke
                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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                                                                                                                                                                                                                                               TYPE: DNA
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TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
TITLE OF INVENTION: IN PLANT CELLS
TITLE OF INVENTION: IN PLANT CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria
STREET: United States
LIF: 22313-1404
COMPUTRY: United States
LIF: 22313-1404
COMPUTRY: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/453,104
FILING DATE:
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US-08-694-824-23
; Sequence 23, Application US/08694824
; Patent No. 5877306
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Sequence 1, Application US/08817188

Patent No. 6074876

GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION UNBER: US/08/817,188

CURRENT FILING DATE: 1997-05-15
EARLIER FILING DATE: 1996-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((97)...(330))
OCHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4876))
OCHER INFORMATION: PTA.29 promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: prompter region of Rubisco small subunit gene of
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KET: misc_feature
LOCATION: Complement((2658)..(3031))
OCHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.6%; Score 189.6; DB 3;
99.5%; Pred. No. 6.8e-35;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: Complement((4922)..(4946))
OTHER INFORMATION: LB: T-DNA left border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: NAME/KEY: misc_feature
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LOCATION: Complement(()
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4946
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                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                   APPLICANT: CORNELISSEN, Marc
APPLICANT: SOTARRY, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKK, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                   ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "Nucleotides 2078-2082; OTHER INFORMATION: wherein N is not known." US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No. 6.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SOD ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3200 base pairs
                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 2078..2082
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3132 GACCATGTAC 3141
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION:
GENERAL INFORMATION:
FILE REFERENCE: 2121-01279
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT PILING DATE: 1997-05-15
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1996-07-31
SERLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VOR. 2.0
SEQ ID NO 5
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (2).
COCHER INFORMATION: PT1B6S3
OTHER INFORMATION: PT1B6S3
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LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (84)..(296)
OTHER INFORMATION: 3' 97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of
OTHER INFORMATION: the ST-LSI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (3059)..(5056)
OTHER INFORMATION: uidA: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (318)..(869)
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08817188 Patent No. 6074876
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FALUNCA:

NAME/KEY: misc_feature

LOCATION: (5058)..(5059)

OTHER INFORMATION: region with unknown sequence (may contain up to 20 of the Information: color).

NAME/KEY: misc_feature

LOCATION: (5077)..(5078)

OTHER INFORMATION: region with unknown sequence (may contain up to 20 of the Information: region with unknown sequence (may contain up to 20 of the Information: unclectides)

NAME/KEY: misc_feature

LOCATION: (5476)..(5479)

OTHER INFORMATION: region with unknown sequence (may contain up to 20 of the Information: region with unknown sequence (may contain up to 20 of the Information: region with unknown sequence (may contain up to 20 of the Information: region with unknown sequence (may contain up to 20 of the Information: nucleotides)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                 NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
OTHER INFORMATION: pTIB6S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 5560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SORTHERY, MAIC
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOKKY, Jan
APPLICANT: VAN AARSSEN, ROel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
LOCATION: (5067)..(5502)
OTHER INFORMATION: P35S: 35S promoter region of CaMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
45.6%; Score 189.6; DB 3;
Best Local Similarity 99.5%; Pred. No. 6.9e-35;
Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERRY SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STAME: Virginia Under STAME: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-016-23
; Sequence 23, Application US/08232016
; Patent No. 5925547
; GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORNELISSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 gaccatgtac 190
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/note= "Coding region of a truncated bt2 (cryIAb) gene, also designated as the bt884
                                                                                                                                          1881 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 1940
                                                 61 atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
                                                                      MODIFIED GENES AND THEIR EXPRESSION IN
PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: plasmid DNA designated as pJD884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08232016 Patent No. 5952547 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6201
INFORMATION FOR SED ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SOETAERT, Plet
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSSEN, ROel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MC
TITLE OF INVENTION: PL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                              2061 GACCATGTAC 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                               181 gaccatgtac 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                 US-08-232-016-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 3582..4407
UNTER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1793...2026
PTER INFORMATION: /notte= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "Coding region of a truncated modified bt2 (cryIAb) gene, also designated as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 7071...7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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| NAME/KEY: misc_feature
| LOCATION: 5600..6457
| OTHER INFORMATION: /note= "Sequence complementary to
| Patent No. 5952547
| OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
COGATION: 2396.2921
COTHER INFORMATION: /note= "355 promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 189.6; DB 2;
Pred. No. 7.1e-35;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: plasmid DNA designated as pPS0212
                                                                                                                                                                                                             NAME: MCGOWAN, MALCOLM K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPRA: (703) 836-5021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7566 base pairs
               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
RILING DATE: 30-CCT-1991
PRIOR APPLICATION NUMBER: GB 92400820.4
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: crylab6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
03-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.1785
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY: misc_feature

1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60

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NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
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                                                                                                                                                                                                                                                                                                                                                  LUCCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco (OTHER INFORMATION: Arabidopsis (Pssu)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement:
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
45.2%; Score 188; DB 3; Length 5864;
Best Local Similarity 98.9%; Pred. No. 1.6e-34;
Matches 188; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                 LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                         NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KRET: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (5217)...(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
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LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of
OTHER INFORMATION: amyloliquefaciens
                                 OTHER INFORMATION: plasmid pTC0113
                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement()
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                                                                                                                                                                                                                                                        LOCATION: 3006..3665
OTHER INFORMATION: Chloramphenicol acetyl transferase gene."
OTHER INFORMATION: Chloramphenicol acetyl transferase gene."
FEATURE:
NAME/KEY: misc.feature
LOCATION: 3666.4491
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                        /note= "3' regulatory sequence
containing the polyadenylation site derived from Agrobacteriu
T-DNA gene 7."
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LOCATION: 5684..6541
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1965 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 2024
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99.5%; Pred. No. 7.1e-35;
tive 1; Mismatches 0; Indels 0;
                                                                                                                                                LOCATION: 2480_.3005
OTHER INFORMATION: /note= "355 promoter sequence
OTHER INFORMATION: derlyed from Cauliflower mosaic virus."
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ORGANISM: Artificial Sequence
PERTURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

1.0CATION: 7155..7639

2.0THER INFORMATION: /note= "TR1' and TR2' promoter

3.9CHER INFORMATION: derived from Agrobacterium T-DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
LENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08894440 Patent No. 6025546
OCHER INFORMATION: /not
OTHER INFORMATION: /not
OTHER INFORMATION: CODE
OTHER INFORMATION: T-DN:
                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.5
Matches 189; Conservative
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APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Plet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: OCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3025 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING APPLICATION 1536
PRICATION NUMBER: US 07/937,869
FILING APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 18-APR-1990
ATTORNEY AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REGISTRATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COATION: 2151..2155
COTHER INFORMATION: /note= "Nucleotides 2151-2155";
COTHER INFORMATION: wherein N is not known."
US-08-694-824-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 176.6; DB 2;
Pred. No. 5.7e-32;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          Sequence 22, Application US/08694824
Patent No. 5877306
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
rocation: 2151..2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.5
Best Local Similarity 99.4
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS ADDRESSE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                 RESULT 14
JS-08-694-824-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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                                                                                                                                                          APPLICANT: CORNELISSEN, Marc
APPLICANT: SCRTAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: Alexandria
STREET: George Mason Bidg., Mashington & Prince Sts.
CITY: Alexandria
STAME: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3025 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3085 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 3144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 5.7e-32;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

: LOCATION: 2151..2155

: OTHER INFORMATION: /note= "Nucleotides 2151-2155

: OTHER INFORMATION: wherein N is not known."

US-08-453-104-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22313-140.

COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REGISTRATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          Sequence 22, Application US/08453104 Patent No. 5633446 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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COUNTRY: United States
ZIP: 22313-1404
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Best Local Similarity 99.4
Matches 176; Conservative
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181 gaccatgtac 190
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                     63 GACCATGTAC 54
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UI-M-BH1-AU068795 wb84b08.x

at17b03.x AV193861

UI-M-AIO-ZU45b04.r q166h07.x UI-M-AIO-

AV670633 mq21b05.r xz99d05.x

we29a10.x EST270918

BB283443

Perfect score:

Sequence:

nucleic

е 6

Run

Scoring table:

Searched:

0B 0B

Minimum Maximum

Database

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Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota, metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Eukaryota, wetazoa; Nematoda; Caenorhabditis.

1 (bases 1 to 568)
Reboul,J., vadilo,p., Tzellas,N., Thierry-Mieg,N., Moore,T.,
Zackson,C., Shin-i,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Ere,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
                                                                                                                                                        AL428079 clone BAO
BG220991 602386981
BF311402 601896616
AW425779 58291 MAR
BB464829 BB464829
AA466153 v973305.r
C26671 C26671 Rice
AV181598 AV181598
AI880854 at17503.x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Jerome_Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted profein encoding ORF. C. elegans ORFeome
cloning project: Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BII74209 568 bp mRNA EST 09-JUL-2001 OSTF0118FB_1 AD-WIMCDNA Caenorhabditis elegans cDNA similar to BII74209
                                                                                                                                                                                                                                                                                                       AV193861 AW04893 LAW04893 LAW06879 AL06879 AL068708 LAM1835705 LAM17833 AA175018 GBE5528 AV670633 AA124200 m
                                                                                                          AZ187379
AQ946406
BF527305
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AQ948016
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BB283443
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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180

Fax: 617 632 2425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                            AZ187379
AQ946406
BF527305
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C26971
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AI880854
AV193861
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AU068795
AI669082
AI835705
AA478333
AI275018
BE859284
                                                                                                                                                           CNS073X5
BG290991
                                                                                                                                                                                                         AW425779
BB464829
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AA124200
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1. .568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Reboul J, Vaglio P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI174209.1 GI:14640012
                                                                             Nat. Gene
21135099
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\begin{array}{c} 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.2.5\\ 2.
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BI174209/c
LOCUS
DEFINITION
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COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
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BG563856 602584663
AQ256131 nbxb0015D
AW370342 RC1-BT025
BE150747 RC1-HT026
BF589714 naa08h06.
AI562674 TENS2662
BE87550 7901f06.x
H66110 yr70h02.r1
H66097 yr70e02.r1
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                                                                                                                           (without alignments)
95.360 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             Search time 2253.73 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                        22703874
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                        11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                          December 19, 2001, 16:22:38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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BG563856
AQ256131
AW370342
BE150747
BF589714
AI562674
BE857550
H66110
AQ48334
H66097
                                                                             nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_gss_hum: *
em_gss_inv: *
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em_gss_rod:*
em_gss_vrt:*
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20
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seq length: 2000000000
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em_estov:*
em_htc:*
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gb_est2:*
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2212
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1170
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3325
3418
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4433
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Match
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17.4 116.8 116.8 116.8 116.8 115.8 115.8 115.8 115.8

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                                                             20
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
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AQ256131/c
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/Organism-"Homo sapiens"
/db_xref-"taxon:9606"
/db_bost="Human fetal heart, Lambda ZAP Express"
/lab_bost="E. col1 XL1-Blue"
/lab_bost="E. col1 XL1-Blue
                                                      /db_xref="taxon:6239"
/clone_lib="AD-wrmcDNA"
/sex="Hermaphrodite and male"
/tissue_type="mixed stage"
/fote="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA090232 212 bp mRNA EST 24-OCT-1996 chp0019.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens AA090232 GI:1636716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, MSGLL5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.4; DB 11; Length 568;
Pred. No. 2.3e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRIMEES
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTCAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
LOCALLOn/Qualifiers
/organism="Caenorhabditis elegans"
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90.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: liewcceutcc.utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNAs from fetal heart (1996)
Unpublished (1996)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.08;
94.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ctacggcaatgtaccagct 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Conservative
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Fax: 4169785650
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Matches 18: Conserv
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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ORIGIN
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Gaps

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Indels

1 ctacggcaatgtaccagctg 20

Conservative

Best Local Similarity Matches 18; Conserv

Length 212;

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/u.yanism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAbace:4712630"
/clone="InAbace:4712630"
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Sfil (ggcgcctcggcc); Site_2: Sfil (ggccattaggcc); Site_2:
Sfil (ggccatcaggcc); Site_2: Site_1:
Sfil (ggccatcaggcc); Site_2: Site_2:
Sfil (ggccatcaggcc); Site_2: Site_2:
Sfil (ggccatcaggcc); Site_2: Site_2:
Sfil (ggccatcaggcc); Site_2: Site_2:
Sfil (ggccatcaggcc); Site_2: Site_2:
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                    602584663F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4712630 5', BG563856
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Library Oryza sativa genomic clone
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90.0%; Pred. No. 4.7e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ256131 700 bp DNA nbxb0015D03r CUGI Rice BAC L nbxb0015D03r, DNA sequence.
                                                                                                                                                                                                                                                                                                                                               BG563856.1 GI:13571508
116 CTCCGGCAATGTACCATCTG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ256131 GI:3780613 GSS.
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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KEYWORDS
SOURCE
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TITLE

COMMENT

REFERENCE AUTHORS source

FEATURES

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1...170
/organism="Homo sapiens"
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/db_artef="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 618)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +56-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCI-HT0269-010 300-014-h02&t3=2000-03-01&t4=1)
                                                                                                                          Tel: +55-11-2704922

Fax: +55-11-2707001

Bmail: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2-RC1-BT0255-
181099-012-160&t3-1999-10-18&t4-1)

Seq primer: puc IB forward

High quality sequence stop: 170.
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RCI-HF0269-010300-014-h02 HT0269 Homo sapiens CDNA, mRNA sequence.
BEI50747
   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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100.0%; Pred. No. 8.9e+02;
ive 0; Mismatches 0;
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Best Local Similarity
Matches 16; Conserv
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MEDLINE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
BE150747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xrefe='taxon:4530"
/db_xrefe='taxon:4530"
/clone='nbxb0015D03r"
/clone='nbxb0015D03r"
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/lab_nost='E. coll DH10B"
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/note='vector: pBeloBAC11; Site_1: HindIII; Site_2:
/note='vector: pBeloBAC11; Site_1: HindIII; Site_2:
/note='vector: pBeloBAC11; Site_1: HindIII; Rice is one of two most popular grains in the
world: Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocctyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumquanthan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryas astiva, Nipponbare variety. The
library from Oryas astiva, Nipponbare variety. The
close coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 170)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)

Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 700)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Pred. No. 7e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 152.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain-"Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW370342.1 GI:6874996
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94.48;
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Best Local Similarity 94.4
Matches 17; Conservative
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DEFINITION

AW370342

RESULT

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ACCESSION VERSION KEYWORDS

BASE COUNT ORIGIN

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Gaps

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89.5%;
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Best Local Similarity 89.59
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cruzi
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Best Local Similarity
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AI562674
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ORIGIN
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BE857550/c
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                                                                                                     /organisme"Homo sapiens"
/db_xref='taxon:9606"
/dloxref='taxon:9606"
/clone=lib-"H70269"
/dev_stage="Addilf"
/note="Organ: head_neck; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A min1-library was made by cloning products
derived from ORESTES POR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUCl 8 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
27 a 121 c 106 g 164 t
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutherla: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 325)

NII-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NII-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

Confact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CON distribution: N.I.-CGAP clone distribution information can be infoetimage llni.gov

Infoetimage llni.gov

Trace considered overall poor quality

Frace considered overall poor quality

Frace considered overall poor quality

High quality sequence stop: 1.

Ince 1 225
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//dev_atage="adult"
/lab_host="DH10B"
//note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_PT22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF589714 325 bp mRNA EST 12-DEC-2000 namoB0h06.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3254267 3/similiar to TR:099829 Q99829 COPINE I. ;/ mRNA sequence.
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100.0%; Pred. No. 1.1e+03;
.1ve 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:3254267"
/clone_lib="NCI_CGAP_Pr28"
Seq primer: puc 18 forward
High quality sequence start: 50
High quality sequence stop: 617.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 16; Conservative
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="r. cruzi epimastigote normalized cDNA Library"
/cell_type="epimastigote"
/note="colnA library constructed with oligo dT primed
epimastigote mRNA and cloned in pt7t318D phagemid with
modified polylinker (PHARMACIA)" 6 others
reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo.)
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7g01f06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3305219 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24 cgp(1650) San Martin, Prov. de BS AS. Argentina Tel: (54-1)752-9539 or (54-1)752-0021 Fax: (54-1)752-0021 or (54-1)752-9639 Email: dsanchez@inti.gov.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 390)
Verdun, N.E., Di Paolo, N.C., Urmenyi, T.P., Rondinelli, E., Frasch, A.C.C. and Sanchez, D.O.
Gene discovery through expressed sequence tag sequencing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                         79.0%; Score 15.8; DB 11;
89.5%; Pred. No. 1.2e+03;
11ve 0; Mismatches 2;
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Pred. No. 1.3e+03;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Trypanosoma cruzi"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 433)
Mahairas,G.G., Mallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rklh,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 356
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: MISRPI
High quality sequence stop: 356.
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ438334 433 bp DNA GSS 31-MAR-1999
HS_5131_A1_C08_SP6E RPCI-11 Human Male BAC Library Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 11; Length 433;
Pred. No. 1.3e+03;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic clone Plate=707 Col-15 Row-E, DNA sequence.
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GSS.
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89.5%;
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Contact: Wilson RK
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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yr70h02.r1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:210675 5' similar to gb:X69970_cds1 TYROSINE-PROTEIN KINASE H8K (HUMAN);, mRNA sequence.
                                                                                                                                            The seas 1 to 418)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.gov/ncicgap.
CGAP/RTGAP), Tumor Gene Index
Unpublished (1988), Tumor Gene Index
COntact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 433) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 to TR:Q9VKF0 Q9VKF0 CG14939 PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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onaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualiflers
                                     BE857550.1 GI:10371688
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Duncy 20539644
Contact: Erika Asamizu
Contact: Erika Asamizu
The First Laboratory for plant Gene Research
The First Laboratory for Chipa 292-0812, Japan
Kazusa Daya, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii
Ebkaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 454)
Asamiacu. E., Mura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Generation of expressed sequence tags from low-CO2 and high-CO2
DMA. Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                                                                                               79.0%; Score 15.8; DB 11; Length 438; 89.5%; Pred. No. 1.3e+03; 1.ve 0; Mismatches 2; Indels 0.
                                                                        /clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 10;
Pred. No. 1.3e+03;
); Mismatches 2;
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                  /db_xref="GDB:3783491"
                                    /db_xref="taxon:9606"
/clone="IMAGE:210650"
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/db_xref="taxon:3055"
/clone="HC010b05_r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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Matches 17; Conservative
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Edwaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 438)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Mucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,The Washu-Warck Est Project
Unpublished (1995)
Contact: Wilson RK
                        Email: jwallace@u.washington.edu
Glones are derived from the human BAC library RPCI-11. For BAC
Glones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
http://www.htsc.washington.edu
Plate: 707 row: E column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPD097 438 bp mRNA EST 18-OCT-1995
Yr70e02.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:210650 5' similar to gb:x69970_cds1 TYROSINE-PROTEIN KINASE
HG6097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@atson.wustl.edu
High quality sequence stops: 348
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: MI3Rpl
High quality sequence stop: 348.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.3e+03;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                          1. .433
/organism="Homo sapiens"
/db_xref='taxon.9606"
/clone='plate=707 Col=15 Row=E"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                   High quality sequence stop: 433.
Location/Qualifiers
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/organism="Homo sapiens"
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89.5%;
rax: (206) 616-3887
Email: 4wall
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15-DEC-2000

RESULT 14 BF009521/c LOCUS

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REFERENCE AUTHORS

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TITLE JOURNAL

COMMENT

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1. .602
/organism="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/db_xref="taxon:5691"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/note="Vector: pUCIB: Site=1: SmaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University press. 19491."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma.

1 (bases 1 to 602)

1 Sases 1 to 602)

1 El-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Uilu, E., Meiville, S., Donelson, J., Fraser, C. and Adams, M.

Petermination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
Unpublished (1999)

Other, GSSs: Sheared DNA 10586.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through Research Genetics, Alabama, USA. Sheared DNA
end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: Ml3-Reverse
                                                                                                                                                                                                                                                                           A2215252 602 bp DNA GSS 09-JUN-2000
Sheared DNA-105B6.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-105B6, DNA sequence.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Pred. No. 1.3e+03;
0; Mismatches 2;
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Press, 1999)."
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AZ215252.1 GI:8432975
                                                                           337 CTACAGCAATTTACCAGCT 319
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                                       1 ctacggcaatgtaccagct 19
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                              AZ215252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                             RESULT
                                                                                                     qq
                                       ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Another "Vector: pBluescript II SK+; Site_I: ECORI; Site_2:
XhOI; The CDNA library was constructed from mRNA isolated
from the epicotyls of 2 week old seedling for the cultivar
Williams. The seedlings were germinated in a growth
chamber, excised above the soil level, and the plants
were placed in a 100 ppm solution of auxin for 24 hours
prior to harvesting. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dr)
sequence with a XhoI restriction site. ECORI adapters
were ligated to the blunt-ended cDNA fragments followed
by XhoI digestion. The CDNA fragments were directionally
cloned into the ECORI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into BHUB host cells (GibcoBKL). This
                                                                                                                                                                                                          BF009521 472 bp mRNA EST 06-OCT-2000
ss91h03.yl Gm-c1064 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryopta, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GENOME SYSTEMS CLONE ID: Gm-c1064-1518"
/clone_lib="Gm-c1064"
/tissue_type="seedling epicotyls"
/dev.stage="2 week old"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
/cultivar="Williams"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                           Gm-c1064-1518 5', mRNA sequence
BF009521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 g
                                                                                                                                                                                                                                                                                                                                               BF009521.1 GI:10709797
326 TACGGCATTTTACCAGCTG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                    soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine.
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source

FEATURES

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Gaps

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BASE COUNT

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on:

December 19, 2001, 16:22:43 ; Search time 230.16 Seconds (without alignments) 74.498 Million cell updates/sec

US-09-698-903B-7 20

1 ctacggcaatgtaccagctg 20 Perfect score: Sequence:

IDENTITY_NUC Gapox 1.0 Scoring table:

1861242 Total number of hits satisfying chosen parameters:

930621 seqs, 428662619 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_1101:* Database

/SIDSB/gcgdata/geneseq/geneseqn/Nal980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Nal981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Nal981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Nal982.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqn/Nal989.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqn/Nal989.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqn/NA1992.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1993.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1994.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1997.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1997.DAT:*/SIDSB/gcgdata/geneseq/geneseqn/NA1998.DAT:* /SIDS8/gcgdata/geneseg/genesegn/NA1999.DAT: /SIDS8/gcgdata/geneseg/genesegn/NA2000.DAT: /SIDS8/gcgdata/geneseg/genesegn/NA2001.DAT: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pps029 Bt ICP codinpvR36 Bt ICP codinpvR36 Bt ICP codinprasmid DV130 compression DV133 used	Figure 7.15% used Nucleotide sequenc T-DNA of plasmid p Nucleotide sequenc Plasmid pTS172delt	T-DNA of pTTS24. Plasmid pTCO113 T- Plasmid pTCO113 T- Chimeric T-DNA of	Chimeric T-DNA of E. coli plasmid pT Plasmid pTS174 use Plasmid pTS172 use C E. coli plasmid pT Plasmid pTS346. U Plasmid pTS346. U Plasmid pTS346. U	Nucleofide sequenc Plasmid pJD884 con Sequence of opine Complete nucleotid Transformed Arabid Right flanking reg T-DNA right border PCR primer for the PCR primer for the	Nucleotide sequenc Human cDNA sequenc Enterococcus faeca
AAQ14529 AAQ15144 AAZ29121 AAZ29124					AAA59486 AAH18238 AAX13108
3201 12 3201 12 3336 21 3694 21	4832 22 4832 22 4946 18 4946 22 5228 22		5865 22 6539 21 6548 17 6548 18 6548 21 7492 22 7566 14		1290 21 4828 22 1871 20
1000.000.000.000.0000.0000.0000.0000.0000	0.000.000000000000000000000000000000000			100.0 1100.0 1000.0 95.0 90.0 90.0 79.0	
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12 13 14 15	c 17 c 18 c 19	c 21 22 23 24	o 25 2 2 2 2 2 2 3 3 3 3 3 5 3 5 5 5 5 5	0000 0000 00000 000444 00000	0 444 5

ALIGNMENTS

Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barnase gene; PCR primer; ss. PCR primer for the right border in transgenic plant MS-BN1. (AVET) AVENTIS CROPSCIENCE NV. BP. 99US-0457037. De Beuckeleer M; 06-DEC-2000; 2000WO-EP12872. AAH25428 standard; DNA; 20 (first entry) WO200141558-A1. 08-DEC-1999; 22-AUG-2001 14-JUN-2001 De Both G, Synthetic. AAH25428; AAH25428 RESULT

Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome WPI; 2001-381419/40.

Example 4; Page 43; 98pp; English.

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Gaps

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Length 20; Indels

6 C; 5 G; 4 T; 0 other;

Sequence 20 BP; 5 A;

X OS

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Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                  WPI; 2001-300517/31.
                                                                                                                         Agrobacterium sp
                                                                                                                               WO200131042-A2
                                                                                                 06-AUG-2001
                                                                                                                                                 29-OCT-1999;
                                                                                                                                    03-MAY-2001.
                                    transgene
                                                                                                                                                             Weston B,
                                                                                          AAD06996;
                                                                                                                   TAIL; 88.
                                                                                 AAD06996
ID AAD0
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The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic blant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..234
/*tag= a
/note="Corresponds to plant DNA"
235..415
                                                                                    DB 22;
0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                             Mismatches
                                                                                    Score 20;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 51; 53pp; English.
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                                                                                                                                                                                                                                                                                                                   BP.
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≩
                                                                                  100.0%;
llarity 100.0%;
Conservative 0;
                                                                                                                                                                  1 ctacggcaatgtaccagctg 20
                                                                                                                                                                                     1 ctacggcaatgtaccagctg 20
                                                                                                                                                                                                                                                                                       AAD06997/c
ID AAD06997 standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Agrobacterium sp.
Chimeric - Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-2000; 2000WO-EP10680,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                male-sterility gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
`~ 20; Conserv?
                                                                                                     Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weston B,
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                      AAD06997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MS-B2
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                                                                                                                                                                                                                                                                                                                                                                                          ö
The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male sterility gene (e.g. barnase gene), and the other plant has an expression cassette comprising a fertility restorer gene (e.g. barstar gene) integrated into the genome. The fartility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. PCR primers AAH25427-28 were used to amplify the right border of a vector in a transgenic plant which carries the TA29-barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is tertilary thermal interlaced (TAIL)-PCR primer WDB258 used to right (5') and left (3') border flanking region of elitement WS-B2. This primer corresponds to position 224-243 of plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PÇR primer MDB258 to generate the flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; PCR primer; thermal asymmetric interlaced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                           DB 22;
0.26;
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                                                                                                                                                                                                                                                                        Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 28; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD06996 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                         ctacggcaatgtaccagctg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ctacggcaatgtaccagctg
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Gaps

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100.0%; Score 20; DB 22; Length 415; ilarity 100.0%; Pred. No. 0.38; Conservative 0; Mismatches 0; Indels

AAD06999

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The unique BglII-Ort (720-725) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1032-1037) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is transfected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n DNA incorporation; recombinant DNA techniques; plant genome; legumin; B4 gene; signalpeptide; Le-Sig.T7.; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 11; Length 1037; 100.0%; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                             Incorporation of DNA into higher plant genome - by specified recombinant DNA techniques.
                                                                                                                            Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; USP-Pr.T7-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product=Legumin-signalpeptide
                                                                                                                                                                                                                                                                                                                           Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legumin-signalpeptide cassette Le-Sig.T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           χ,
                                                                                                  USP-Promoter-cassette USP-Pr.T7.1.
            BP.
                                                                                                                                                                                                                                                                                                                           Baumlein H, Muntz
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            AAQ04705 standard; DNA; 1037
                                                                                                                                                                                                                                                                88DD-0319887.
                                                                                                                                                                                                                                   89DE-3920034
                                                                                                                                                                                                                                                                                            (PFLA-) VE KOMB PFLANZENZUC
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747..814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-172459/23
                                                                                                                                                                                                                                   20-JUN-1989;
                                                                                                                                                                                                                                                                19-SEP-1988;
                                                                     12-OCT-1990
                                                                                                                                                                         DE3920034-A
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                                                                                                                                                                                                                                                                                                                           Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ04703;
                                         AAQ04705;
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AAQ04705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                   MS-B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 22; Length 416; 100.0%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                    Left (3') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Corresponds to plant DNA"
                                                                                                                                                                                                                                                                                                                            /"cag" a
/note= "Corresponds to T-DNA"
194..416
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 52; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AVET ) AVENTIS CROPSCIENCE NV.
            - Agrobacterium sp.
- Brassica sp.
                                                                                                              AAD06999 standard; DNA; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Beuckeleer M;
                                                                                                                                                                       06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                  male-sterility gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200131042-A2
                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weston B,
                                                                                                                                                                                                                                                                            Chimeric
Chimeric
                                                                                                                                           AAD06999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Gaps

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Indels

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89DE-3920034

20-JUN-1989;

RESULT

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Gaps

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Indels

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us-09-698-903b-7.rng

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ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1155-1160) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected. See also AAQ04703-Q04706.
                                                                                                Score 20; DB 11; Length 1160;
Pred. No. 0.43;
Mismatches 0; Indels 0
                                                                 Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                 USP-Promoter-cassette USP-Pr.T7.2.
                                                                                               100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                       AAQ04704 standard; DNA; 1166 BP
                                                                                                                                   89DE-3920034.
                                                                                                                                                                                                                                                                                                                                                                           88DD-0319887.
                                                                                                                                                                                                                                                                                                                                                                                             (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                               (first entry)
                                                                                            Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-172459/23.
                                                                                                                                                                                                                                                                                                                                                        20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1988;
                                                                                                                                                                                                                                                                                                               DE3920034-A.
                                                                                                                                                                                                                                              12-OCT-1990
                                                                                                                                                                                                                                                                                                                                    31-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                 Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transfected
                                                                                                                                                                                                                          AAQ04704;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                     RESULT
AAQ04704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
        8.588888
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                                                                                                                                              for
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                    The Legumin gene B4 is used. The unique BgIII-Ort (815-820) site is ligating foreign DNA and the HindiII-Ort in the 3' polylinker (1080-1085) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected.
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                      100.0%; Score 20; DB 11; Length 1085; 100.0%; Pred. No. 0.43; 0; Mismatches 0; Indels 0
                                                                                     Incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incorporation of DNA into higher plant genome - by specified recombinant DNA techniques.
                                                                                                                                                                                                         Sequence 1085 BP; 368 A; 219 C; 155 G; 343 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; signalpeptide; USP-Sig.T7.; ss.
                                           Wobus U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wobus
                                          Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product=signalpeptide
747..817
                                                                                                                                                                                                                                                                                                                                                                                                        USP-signalpeptide cassette USP-Sig.T7.
                                        Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
708..877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bassuner R, Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                          88DD-0319887
                                                                                                                                                                                                                                                                                                                                              AAQ04706 standard; DNA; 1160
                   (PFLA-) VE KOMB PFLANZENZUC
                                                                                                  recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89DE-3920034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                        Baumlein H,
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                    Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ; pp; German.
                                                          WPI; 1990-172459/23.
P-PSDB; AAR05198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-172459/23.
P-PSDB; AAR05199.
19-SEP-1988;
                                      Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE3920034-A.
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                                                                                                                                                                                                                                                                                                                                                                  AAQ04706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The unique BglII-Ort (720-725) site is for ligating foreign DNA and HindIII-Ort in the 3' polylinker (1261-1266) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                               Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; USP-Pr.T7-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1166 BP; 381 A; 208 C; 196 G; 381 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 11; 100.0%; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Incorporation of DNA into higher plant genome recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ25707 standard; DNA; 1186 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ25707;
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ID AAQ2
XX
AC AAQ2
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The unique BglII-Ort (890-895) site is for

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region containing polyadenylation signal of gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The HindIII-ECORI fragment (AAT39337) of plasmid pTS88 contains barstar DNA under control of a 35S promoter. The plasmid was used with pTS174 (see also AAT39336) contg. barnase DNA under control of the stamen specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVE136 (see also AAT39388) contg. barnase DNA under control of the stamenspecific PCA55 promoter to produce male sterile maize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible
                                                                                                               Jorgan b
/Label= P35S
/function= 35S promoter of cauliflower mosaic virus
/function= Strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of male sterile plants by transforming with a chimaeric construct - comperising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
 transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 17; Length 1303;
Pred. No. 0.44;
Mismatches 0; Indels 0;
                                                                                                                                                                                                          /product= Bacillus amyloliquefaciens barstar
968..1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            low level expression of barnase DNA in non-stamen tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                                               /label= pgEM2
/note= "polylinker of pgEM2"
                                                                                                                                                                                                                                                                                                                       /note= "polylinker of pGEM2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michiels F;
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 38; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ž
                                                                                                                                                                                    /*tag= c
/label= barstar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                /*tag= e
/label= pGEM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cornelissen M,
                                                                                                                                                                                                                                  /*tag= d
/label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                               96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                      95EP-0400364
                                                                                                                                                                                                                                                          /function=
                                                                                                                                                                                                                                                                                  1288..1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                         *69*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-402373/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (PLBZ ) PLANT
                                              Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3otterman J,
                                                                                                                                                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                               WO9626283-A1
                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1996
                        Synthetic.
                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1098
                                                                                                                                                                        CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Two transformed corn plants were analysed by means of Southern hybridisation. As a probe, a 1184 bp EcoRT-HindIII fragment derived from another plasmid was used. The sequence of that plasmid is given below. Results showed that at least a chimeric neo gene was
                                                         Nicotiana tabacum; neomycine phosphotransferase; Agrobacterium; ss.
                                                                                                                                   a
"sequence derived from tapetum specific
promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming monocotyledonous plants e.g. cereals - comprises wounding and/or degrading cells of intact plant tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
                                                                                                                                                                                                                               3' regulatory sequence contg. the polyadenylation site derived from Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                           /product- neomycine_phosphotransferase 791..1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1186 BP; 244 A; 317 C; 325 G; 300 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 13
100.0%; Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                integrated into the plant genomic DNA
                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 60; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                 91WO-EP02198
                                                                                                                                                                                                                                                                                                                                                          90EP-0403332
91EP-0401888
                                                                                                                                                                                                                    /*tag= c
/note= "3'
           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                    gene probe
                                                                                                                                   /*tag=
                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                      Dhalluin K, Goebel E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-217075/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                embryogenic callus
                                  Chimeric neo
                                                                                                                                                                                                          misc_feature
           07-DEC-1992
                                                                                                                                                                                                                                                                                                                                 21-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                          23-NOV-1990;
08-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-1997
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                                                                                                                                                                                                                                                                                  WO9209696-A
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                                                                                 Synthetic
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                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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ID AAT3
XX
AC AAT3
XX
DT 22-J
XX
XX
XX
KW Plas
                                                                                                          Key
                                                                                                                                                                      CDS
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Gaps

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pPS029 Bt ICP coding sequence.
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  coding sequence
                                                                                                                                                                                                                          Cornelissen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cornelissen M,
                                                        deletion; ss
                                                                                                                                                  17-APR-1991;
                                                                                                                                                                            18-APR-1990;
                                                                                                     WO9116432-A
                                                                                                                             31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deletion; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-1991;
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                                                                               Synthetic.
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        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                       Transgenic seed; marker; aleurone-specific promoter; Plasmid DV131; GFP:NPTII fusion protein construct; L3/EGFP:NPTII/Tr7; maize R gene; expression cassette; maize L3 oleosin gene; chimeric gene; transgene; MGFP:NPTII translational fusion; Tr7 terminator; Luciferase gene; assay; Green fluorescent protein; GFPP; gene fusion; selection; screening; expression; automated seed screening technique; screenable marker; transformant; embryogenic tissue; implementation; ds.
                                                                                                                                                                                                                                                                                                                                                                                               Screenable marker genes useful for identification of transgenic seeds for plant breeding -
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                                                                                Plasmid DV131 comprising L3/EGFP:NPTII/Tr7 expression cassette.
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Pred. No. 0.49;
; Mismatches 0; Indels 0
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           AA229122 standard; DNA; 3153 BP.
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                                                                                                                                                                                                                                                                             99WO-US11023
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                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                 Kriz AL, Spencer TM;
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Matches 20; Conserv
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                                                                                                                                                                                                     Synthetic.
                                   AAZ29122;
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AAZ29122
ID AAZ2
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ID AAQ1
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AC AAQ1
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Gaps
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PPSO29 is identical to pVE36 (AAQ15144), but carries both the amino-
terminal modification and the internal modification of the Bt ICP
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                                                                                                                                                                                                                                                                                                                                                                                                 Modified Bacillus thuringlensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
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Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis; insecticidal crystal protein; ICP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6(c); 78pp; English.
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terminal modification and the internal modification of the Bt ICP
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                                                   Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 12; Length 3201; 100.0%; Pred. No. 0.49; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3201 BP; 915 A; 651 C; 700 G; 930 T; 5 other;
                                                                                                                                                                                                                                                sequence refers to not known nucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ctacggcaatgtaccagctg 20
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pPS029 (AAC
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The present DNA sequence is the plasmid DV133, comprising
13/rACTI intron/EGFP:NPTII/Tr7, that is used in the generation of
13/rACTI intron/EGFP:NPTII/Tr7, that is used in the generation of
13/rACTI intron/EGFP:NPTII/Tr7, that is used in the generation of
14 comprising, a promoter from the maize L3 oleosin gene, the rice actin 1
15 intron, the coding sequence of EGFP:NPTII translational fusion, excised
16 from DV126 and the Tr7 terminator. This plasmid is used to carry a
17 chimeric gene, comprising an aleurone-specific promoter like L3, that is
18 chimeric gene, comprising an aleurone-specific promoter like L3, that is
18 chimeric gene, comprising an aleurone-specific promoters of the gene fusions
18 chimeric gene, comprising on a screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in
18 chimeric genes, allowing selection and screening of viable transgenic seeds. Screening of transgenic seeds avoids the need for growing and assaying of seeds for transgenes and allows implementation
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allow both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in embryogenic tissues, allowing selection and screening of viable transgenic seeds. Screening of transgenic seeds avoids the need for growing and assaying of seeds for transgenes and allows implementation of automated seed screening techniques for the identification of
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                                                                                                                                                                                                                                                     21; Length 3336;
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Pred. No. 0.5;
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of automated seed screening techniques for the identification of transgenic seeds.
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V00090 Agrobacteri
X00431 Agrobacteri
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A60108 Sequence 1
A76915 Sequence 1
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AX172440 Sequence
AX172440 Sequence
A71437 Sequence 7
A60112 Sequence 5
AR098311 Sequence
AX127748 Sequence
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A76916 Sequence 2
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E31990 Mutated bar
A24783 plasmid pPS
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A24782 plasmid pJD
AR074387 Sequence
AR078675 Sequence
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I44103 Sequence 22
AJ251014 Transform
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A10939 Nucleotide
A10943 Nucleotide
A10941 Nucleotide
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A1095107 Sequence
AR095107 Sequence
AR012338 Sequence
I49886 Sequence 2
I82374 Sequence 2
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    /organism="synthetic construct"
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Sequence 7 from Patent WO0131042.
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                1472140 segs, 8248589755 residues
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                                                                                                                  December 19, 2001, 16:22:38;
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Maximum Match 100%
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length: 2000000000
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15-MAY-2001

SUMMARIES

AJ251013 Transform

RESULT AX172448

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FEATURES

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/note="theroretical fusion junction (24) with gene 7 of Ti
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' border flanking region of elite event MS-B2"
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synthetic construct
artificial sequence.
1 (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
Wale-sterile brassica plants and methods for producing same
Male-sterile brassica.
Avents Cropscience N.V. (BE)
Location/Qualifiers
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Ouery Match

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Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Score 20; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels
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              1. .13
/note="beta-1-tubulin sequence"
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                                           14. .28
/note="puc 13 polylinker"
29. .35
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173. .178
/note="put.polyA signal"
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Sequence 10 from Patent W00131042.
AX127757
AX127757.1 GI:14134404
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                                                                                         /note="Sal I linker
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/note="plant DNA"
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/note="T-DNA"
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Location/Qualifiers
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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 249)
Guiltinan,M.J., Velten,J., Bustos,M.M., Cyr,R.J., Schell,J. and
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                                                                                                                                                                                                                                                                                                        synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 20)
de Both, G. and de Beuckeleer, M.
Hybrid winter oilseed rape and methods for producing same Petent: WO 0141558-A 9 14-JUN-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
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                                                                    Length 20;
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Query Match

Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels
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                                                               Score 20; DB 6;
Pred. No. 15;
Mismatches 0;
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/db_xref="taxon:32630"
/note="primer 258"
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/db_xref="G1:4376141"
/translation="AMAWASSNWSTDPPMS"

    .249
    /organism="synthetic construct"
/db_xref="taxon:32630"

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Sequence 9 from Patent W00141558.
AX172448
AX172448.1 GI:14597560
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1 (bases 1 to 878)
McPherson, J.C.
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plasmid.
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Best Local Similarity 100.
Matches 20; Conservative
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/note="unknown gene (148 is 1st base in codon) (525 is 3rd
base in codon)"
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Agrobacterium tumefaciens gene encoding 'transcript 7' mRNA for a
protein with unknown function.
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1 (bases I to 831)

Dhaese, P., De Greve, H., Gielen, J., Seurinck, J., Van Montagu, M.M. and Schell, J.

Identification of sequences involved in the polyadenylation of higher plant nuclear transcripts using Agrobacterium T-DNA genes
                                                                                                                      /organism="synthetic construct"
/db_xref="taxon:32630"
/note="3' border flanking region of elite event MS-B2"
1 .193
                                                                                                                                                                                                                                                                                                                                     Gaps
synthetic construct
artificial sequence.
1 (abass 1 to 416)
Neston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 110 03-MAY-2001;
Aventis Cropscience N V. (BE)
Location/Qualifiers
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Submitted (27-MAY-1983) to the EMBL/GenBank/DDBJ databases
Data Kindly reviewed (27-MAY-1983) by Dhaese P.
Location/Qualiflers
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/strain="(octopine TL-DNA)"
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75. .81
/note="CG [1] revised CCAGAGG [2]"
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/citation=[2]
99. .101
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132. .672
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/sitation=[2]
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unidentified reading frame.
Agrobacterium tumefaciens.
Agrobacterium tumefaciens
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/note="plant DNA"
72 c 54
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2 (bases 76 to 100)
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LYGKGSLSQRIHDTHLKFKERELSFTTIKPAEMKAQQSDLTYYVAIFQSNYFLCVSN
PEKGFLRCHNRPFLXPIVAHGSMS"
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Rhizobiaceae; Rhizobium.
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109. .489
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/note="polyadenylation signal"
189 c 139 g 262 t
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/db_xref="taxon:358"
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Gaps

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RESULT A10942

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/note="sequence derived from tapetum specific promoter of
                                                                                                                                                                                                                                                                                             A10941 1166 bp DNA PAT 27-SEP-1993
Nucleotide sequence 3 from patent number DE3920034.
A10941 GI:492368
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100.0%; Score 20; DB 6; Length 1160;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 20; Conservative 0; Mismatches 0; Indels
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/gene="neomycine phosphotransferase gene"
167. .790
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/db_xref="taxon:32630"
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Location/Qualifiers
1. .1160
/organism="unidentified"
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a 194 c 188 g 411
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Location/Qualifiers
1.1166
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/db_Xref="taxon:32644"
381 a 208 c 196 g 381
                                                                  411
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1. .1186
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Nucleotide sequence 1 from patent number DE3920034.
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Bost Local Similarity 100.0%; Pred. No. 8.7;

Matches 20; Conservative 0; Mismatches 0; Indels
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Matches 20; Conservative 0; Mismatches 0; Indels
                      Nucleotide sequence 4 from patent number DE3920034. A10942. 1 GI:492369
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Nucleotide sequence 5 from patent number DE3920034.
A10943.1 GI:492370
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                                                                                                                                                                  Patent: DE 3920034-A 4 31-MAY-1990;
Location/Qualifiers
1. .1037
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338 a 174 c 166 g 359
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Location/Qualifiers
1.1085
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369 a 218 c 155 g 343
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EHOGIAPAELFARLKARMPGGEDLVVTHGDACLPNIMVENGRESGFIDGGRLGVADR
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1055. .1186
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7"
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/db_xref="GI:4529900"
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D'Halluin, K. and Gobel, E.
Process for transforming monocotyledonous plants
Patent: US 6074877-A 2 13-JUN-2000;
Location/Qualifiers
1. 1186
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D'Halluin,K. and Gobel,E.
Process for transforming monocotyledonous plants
Patent: US 6002070-A 2 14-DEC-1999;
Location/Qualifiers
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317 c 325 g
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TITLE
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/note="coding sequence of neomycine phosphotransferase" 791. .1186
/note="3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA gene
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/note="sequence derived from tapetum specific promoter of
Nicotiana tabacum"

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   6; Length 1186;
                                     Indels
                                                                                                                                                                                                                                                                               synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 1186)
D'Halluin,K. and Goebel,E.D.
Process for transforming monocotyledonous plants
Patent: EP 0955371-A 2 10-NOV-1999;
PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/db_xref="taxon:32630"
/note="DNA used as probe for neo gene"
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Score 20; DB 6,
Pred. No. 8.5;
); Mismatches
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Sequence 2 from Patent EP0955371.
AX012338
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Job time: 3911 sec
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Matches 20; Conservative
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Best Local Similarity
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ORGANISM: probe
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                              Sequence 2, Appli
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41.092 Million cell updates/sec
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                                                                                                                                                                      December 19, 2001, 16:22:43; Search time 110.23 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-475-975-2
US-08-894-440-2
US-08-994-440-2
US-08-68-53-104-23
US-08-64-814-23
US-08-694-814-22
US-08-694-814-22
US-09-080-625-2
US-09-080-625-2
US-08-817-188-1
US-08-817-188-1
US-08-894-440-4
US-08-894-440-1
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Maximum Match 100%
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Sequence 2, P
Sequence 41, P
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Sequence 15,
Sequence 24,
Sequence 24,
                                                                        Sequence 1
Sequence 1
Sequence 1
               Sequence
                                                            Sequence
                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CITY: Alexandria
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: VIrginia
COUNTRY: United States
ZIP: Z2313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOSPY MSS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/064,121

FILING APPLICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 9040332.1

FILING DATE: 23 NOV-1990

PRIOR APPLICATION NUMBER: BP 91401888.2

APPLICATION NUMBER: BP 91401888.2

ATTORNEY/AGENT INFORMATION:

NAME: Crane-Feury, Sharon E

REGISTRATION NUMBER: 010830-043

REFERENCE/DOCKET NUMBER: 010830-043

TELECOMMUNICATION NUMBER: 010830-043
         US-08-726-3064-2
US-08-726-3064-2
US-08-716-942-21
US-08-116-92-21
US-08-483-232-15
US-08-483-140-15
US-08-913-140-15
US-08-910-041-15
US-09-328-474-15
US-09-100-546-15
US-09-100-546-15
US-09-577-758-15
US-09-577-758-15
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US-08-814-095-7
US-09-103-840A-2
US-08-690-495-41
                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08064121
Patent No. 5641664
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1186 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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us-09-698-903b-7.rni

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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                  FEATURE:
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                                                                                                                                                             FEATURE: INTORNATION: PHOSPHOLTANSIETASE GENE"

NAME/KET: -
LOCATION: 186

OTHER INFORMATION: /label= 3'g7

OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium US-08-064-121-2
                                  /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
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100.0%; Score 20; DB 1; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                 /label= NPTII
/note= "coding sequence of neomycine phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08478015
Patent No. 5712135
GENERAL INFORMATION:
APPLICANT: D'HALLIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-088
TELECOMMUNICATION INFORMATION:
TELEFENORE: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                     1033 CTACGGCAATGTACCAGCTG 1052
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                                                             FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
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US-08-478-015-2
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NAME/KEY: -
LOCATION: 9..790
OTHER INFORMATION: /label- NPIII
OTHER INFORMATION: /note- "coding sequence of neomycine phosphotransferase ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : NAME/KEY: -
: LOCATION: 791..1186
: OTHER INFORMATION: /Iabel= 3'g7
: OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylat
: OTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
US-08-478-015-2
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APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STREET: Urgaina
COUNTRY: United States
ZIP: 22313-1404
COMPUTER: Floppy disk
COMPUTER: Elbopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,975
FILING DATE: O'-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 24-MAY-1993
APPLICATION NUMBER: EP 90403332.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08475975 Patent No. 6002070 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1033 CTACGCCAATGTACCAGCTG 1052
                                                                     TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ctacggcaatgtaccagctg 20
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                         NAME/KEY: - LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                               ORGANISM: probe
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NAME/KEY: -
LOCATION: 71.1186
LOCATION: 7.1.1186
COTHER INFORMATION: 7.1.1186
US-09-084-889-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 3; Length 1186; 100.0%; Pred. No. 0.16;
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/note- "coding sequence of neomycine
phosphotransferase gene"
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APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REPERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                         ALIGNADIA CENTRALIONIONIO DE SEGUENTA CARACTERION NUMBER: 36,113
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMNUNICATION INFORMATION:
TELEPAN: (703) 836-620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                   08/064,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08894440 Patent No. 6025546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ctacggcaatgtaccagctg 20
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SEQ ID NO 2
LENGTH: 1303
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Matches 20; Conservative
   PRIOR APPLICATION DATA:
                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..8
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 9..790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-894-440-2
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LOCATION: 71.1186

COTHER INFORMATION: /label= 3/g7

OTHER INFORMATION: /note= "3' regulatory sequence containing the

COTHER INFORMATION: /note= "3' regulatory sequence containing the

COTHER INFORMATION: 7-DNA gene 7"

OTHER INFORMATION: 7-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: D'OBEL, EIKE
APPLICANT: GOBEL, EIKE
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE ADDRESSE: BUTDS, Doane, Swecker & Mathis
ADDRESSEE: BUTDS, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Pr
                                                                   010830-043
                 REGISTRATION NUMBER: 36.113
REFERENCE/DOCKET NUMBER: 0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-5620
TELEFRX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09084889 Patent No. 6074877
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Crane-Feury, Sharon E
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ctacggcaatgtaccagctg 20
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COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: - - CCATION: 9.790
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: probe
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
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US-09-084-889-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Alexandria
CITY: Alexandria
STATE: Virginia
COUPTR: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
; TOPOLOGY: linear
US-09-080-625-3
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                                                                                                                                                                                                                                                                                                           LOCATION: (968]..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3/97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                              NAME/KEY: misc_feature
LOCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 20; DB 3; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09080625
Patent No. 6307123
GENERAL INFORMATION:
APPLICANT: Kriz, Alan L.
APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: IDENTIFICATION
UNMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                         LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                 LOCATION: (1)..(35)
OTHER INFORMATION: POLYLINKER of pGEM2 (PGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hanson, Robert E.
REGISTRATION NUMBER: P-42,628
REFERNICE/DOCKET NUMBER: DEKM:161
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 44-7577
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3153 base pairs
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KET: misc_feature
LOCATION: (1288)..(1303)
CTHER INFORMATION: polylinker of pGEM2
US-08-894-440-2
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EDNESS: double
    NAME/KEY: misc_feature
                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (695)..(967)
                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (968)..(1287
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STRANDEDNESS:
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Sequence 23, Application US/08453104

Sequence 23, Application US/08453104

Patent No. 563346

GENERAL INFORMATION:

APPLICANT: SOFTAERT, Piet

APPLICANT: NOCKX, Jan

TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS

TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

TITLE OF INVENTION: IN PLANT CELLS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSE: Burns, Doane, Swecker & Mathis

STEET: George Mason Bidg., Washington & Prince Sts.
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                                                                 Gaps
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Score 20; DB 4; Length 3153;
Pred. No. 0.18;
; Mismatches 0; Indels
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Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REJESTRATION NUMBER: 010830-032
REFERENCE/TOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHRRACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKY, JAN
APPLICANT: DOCKY, JAN
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
                                                                   APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: IN PECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                       STREET: George Mason Bldg., Washington & Prince Sts.
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ABOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 2151..2155
OTHER INFORMATION: /note= "Nucleotides 2151-2155
OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18 APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-694-824-22
; Sequence 22, Application US/08694824
? Datent No. 5877306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ctacggcaatgtaccagctg 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                 APPLICANT: CORNELISSEN, Marc
APPLICANT: SCORAGET, Piet
APPLICANT: STAM, Marke
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

: LCCATION: 2078..2082

: OTHER INFORMATION: /note= "Nucleotides 2078-2082

: OTHER INFORMATION: wherein N is not known."

US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-A0G-1996
CLASSIFICATION: 536
PRICATION NUMBER: 05 7/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 05 80 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHRACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-453-104-22
; Sequence 22, Application US/08453104
                                                                                                                                                                   Sequence 23, Application US/08694824; Patent No. 5877306; GENERAL INFORMATION:
APPLICANT: CORNELISSEN, MAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2952 CTACGGCAATGTACCAGCTG 2971
                     2952 CTACGGCAATGTACCAGCTG 2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
1 ctacggcaatgtaccagctg 20
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Matches 20; Conservative
                                                                                                                      RESULT 8
US-08-694-824-23
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DB 4; Length 3336;
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Patent No. 6307123
GENERAL INFORMATION:
APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENTION: IDENTIFICATION
UNMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold White & Durkee
STREET: P.O. Box 4433
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold White & Durkee
STREET: P.O. Box 4433
CORRESPONDENCE ADDRESS:
CORRESPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.18;
has 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
FILING DATE:
CLASSIFICATION:
NAME: HANSON, ROBERT E.
REGISTRATION NUMBER: P-42,628
REFERENCE/DOCKET NUMBER: DEKM:161
TELECHONE: (512) 414-7577
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 3336 base pairs
"VPF: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB
100.0%; Pred. No. 0.1
tive 0; Mismatches
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NAME: Hanson, Robert E.
REGISTRAINON NUMBER: P-42,628
REFERENCE/DOCKET NUMBER: DEKM:161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 2862 CTACGGCAATGTACCAGCTG 2881
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTR: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-080-625-5
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-080-625-5
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Patent No. 6307123

GENERAL INFORMATION:
APPLICANT: ALAN L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENTION: IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 10
CORRESPONDE
                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria a CITY: Alexandria a COUNTRY: United States ZIP: 22319-1404
COUNTRY: United States ZIP: 22319-1404
COMPUTER READABLE FORM: WEDIOM TYPE: Floppy disk COMPUTER: PATORY STEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: PSPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 30,427
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 30,427
FILEROMATION NUMBER: 30,427
FELEROMATION NUMBER: 30,427
FELEROMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 22: LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 20; DB 2; Length 3201;
Bost Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels
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NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3025 CTACGCCAATGTACCAGCTG 3044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ctacggcaatgtaccagctg 20
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: TX
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US-09-080-625-2
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Gaps

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243 CTACGCAATGTACCAGCTG 224
                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                   FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-817-188-5/c
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                                      Gaps
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APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EBARLIER APPLICATION NUMBER: PCT/EP96/03366
EBARLIER FILING DATE: 1996-07-31
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   DB 4; Length 3694;
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                                                                                                                                                                                                                                                APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENTION: IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold White & Durkee
STREET: P.O. Box 4433
                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20;
Pred. No. 0
 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Robert E.
RESISTRATION NUMBER: P-42,628
REFERENCE/DOCKET NUMBER: DEKM:161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 414-7577
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                            Sequence 4, Application US/09080625; Patent No. 6307123; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-817-188-1/C
; Sequence 1, Application US/08817188
; Patent No. 6074876
                                    ;
0
                                                                                          3220 CTACGGCAATGTACCAGCTG 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3403 CTACGGCAATGTACCAGCTG 3422
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 100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3877 base pairs
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-080-625-4
Query Match
Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                            RESULT 13
US-09-080-625-4
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Gaps
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OTHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: Complement((3368)..(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene of
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20;
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SSOFWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4946
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CATTON: Complement((4922)..(4946))

OTHER INFORMATION: LB: T-DNA left border

US-08-817-188-1
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Search completed: December 19, 2001, 17:33:57 Job time: 4274 sec
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                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
FEATURE:
LOCATION: (1)..(25)
OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from OTHER INFORMATION: pTib6S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (84)..(296)
OTHER INFORMATION: 3' 97: 3' untranslated region containing the
OTHER INFORMATION: 90.1yadenylation signal of gene 7 of Agrobacterium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (318)..(869)
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

| LOCATION: (5476)..(5479)

| OTHER INFORMATION: region with unknown sequence (may contain up to 20

| OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of
OTHER INFORMATION: the ST-LS1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
OTHER INFORMATION: pTIB6S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ដ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
FEATURE:
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LOCATION: (3059)..(5056)
OTHER INFORMATION: uidA: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (5058)..(5059)
OTHER INFORMATION: region with unknown sequence (may contain
OTHER INFORMATION: nucleotides)
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LOCATION: (5077)...(5078)
OTHER INFORMATION: region with unknown sequence (may contain
OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (5067)..(5502)
OTHER INFORMATION: P35S: 35S promoter region of CaMV
EARLIER FILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 5
LENGTH: 5560
                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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0
                                        Gaps
                                       ;
0
    Score 20; DB 3; Length 5560;
Pred. No. 0.19;
Mismatches 0; Indels
                                   0; Indels
Query Match 100.0%; S
Best Local Similarity 100.0%; p
Matches 20; Conservative 0;
                                                                              230 CTACGGCAATGTACCAGCTG 211
                                                            1 ctacggcaatgtaccagctg 20
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